

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 07:20:43 ; Search time 3213 seconds
(without alignments)
2393.716 Million cell updates/sec

Title: US-09-758-962-1

Sequence: 1 gtcacgctatcgaataagct.....gaagaagagctcacatg 188

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBdb1:*

- 1: gb_da:*
- 2: gb_hlg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pac:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_da:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_cm:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hlg_hum:*
- 31: em_hlg_inv:*
- 32: em_hlg_other:*
- 33: em_hlg_mus:*
- 34: em_hlg_pln:*
- 35: em_hlg_rod:*
- 36: em_hlg_mam:*
- 37: em_hlg_vrt:*
- 38: em_sy:*
- 39: em_higo_hum:*
- 40: em_higo_mus:*
- 41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	188	100.0	188	6	AX511567
2	181	96.3	181	6	AX511571
3	165	87.8	181	6	AX511573
4	157.4	83.7	1537	14	S68164
5	157.4	83.7	6312	14	TMVRETPC
6	151.4	80.5	180	6	AX511572
7	150	79.8	187	6	AX511569
8	149	79.3	251	6	AX511568
9	138.2	73.5	6311	14	BRU03387
10	119	63.3	2378	14	AB003936
11	119	63.3	6297	14	AB017504
12	117.4	62.4	6298	14	AB017503
13	103.4	55.0	6301	14	AF254924
14	90.4	48.1	798	14	AF187045
15	90	47.9	6303	14	MTVCG
16	88.8	47.2	1543	6	AR220728
17	88.8	47.2	6303	14	ORU30944
18	81	43.1	1536	6	BD137052
19	44	23.4	638	3	AT008367
20	42.2	22.0	749	3	FHE508373
21	41.4	22.0	250029	3	AE014820
22	41	21.8	577	14	AF103781
23	39.4	21.0	5491	6	AX251144
24	39.4	21.0	88824	2	AC144926
25	39	20.7	759	6	E14482
26	39	20.7	2108	5	GG4489221
27	39	20.7	2634	5	D89083
28	39	20.7	7218	6	I66494
29	38.8	20.6	4102	6	AR4775
30	38.8	20.6	4102	6	AR300178
31	38.8	20.6	4102	6	BD058065
32	38.4	20.4	13128	8	AP006073
33	38	20.2	1568	14	MDVFR4
34	37.8	20.1	122	6	AX511570
35	37.8	20.1	259	6	AA4281
36	37.8	20.1	587	6	BD072973
37	37.8	20.1	1094	6	AR168176
38	37.8	20.1	1094	6	E36785
39	37.6	20.0	1490	6	AA1579
40	37.6	20.0	1490	6	AR138332
41	37.6	20.0	1490	6	AR232567
42	37.6	20.0	212535	2	AC128241
43	37.6	20.0	242679	3	AC097122
44	37.4	19.9	6465	3	U41529
45	37.2	19.8	6037	12	YSC2RAM2

ALIGNMENTS

RESULT 1
AX511567
LOCUS
DEFINITION
AX511567
VERSION
AX511567.1
KEYWORDS
SOURCE
ORGANISM
Potato virus X
Potato virus X
Virus; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
REFERENCE
Santa-Cruz,S., Pogue,G.P., Toth,R.L., Chapman,S. and Carr,F.
Expression of foreign genes from plant virus vectors
Patent: WO 02055719-A 1 18-JUL-2002
JOURNAL
BIOSOURCE GENETICS CORPORATION (US)

FEATURES	Location/Qualifiers
source	1. 188
ORGANISM	/organism="Potato virus X"
mol_type	/mol_type="genomic DNA"
db_xref	/db_xref="taxon:12183"
BASE COUNT	66 a 26 c 51 g 45 t
ORIGIN	
Query Match	100.0%; Score 188; DB 6; Length 188;
Best Local Similarity	100.0%; Pred. No. 8.6e-40;
Matches	188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GTGCAGCGGTATCGAATAAGCTTGATATCGAATTCGTCGATTCGGTTCGACGATTTAAAGCG 60
DB	1 GTGCAGCGGTATCGAATAAGCTTGATATCGAATTCGTCGATTCGGTTCGACGATTTAAAGCG 60
OY	61 GTTGACAACCTTTAAAGAGAGAAAAAGAGGTTGAAGAAAAAGGCTGTAGTAAGTAT 120
DB	61 GTTGACAACCTTTAAAGAGAGAAAAAGAGGTTGAAGAAAAAGGCTGTAGTAAGTAT 120
OY	121 AAGTACAGACCGGAGAGAGTACGCCGCTCGATTCGTTAATTGGAAGAGAAAGAGCT 180
DB	121 AAGTACAGACCGGAGAGAGTACGCCGCTCGATTCGTTAATTGGAAGAGAAAGAGCT 180
OY	181 C 181
DB	181 C 181
RESULT 2	
LOCUS	AX511571 181 bp DNA linear PAT 27-SEP-2002
DEFINITION	Sequence 5 from Patent WO02055719.
ACCESSION	AX511571
VERSION	AX511571.1 GI:23392410
KEYWORDS	
SOURCE	Potato virus X
ORGANISM	Potato virus X
REFERENCE	1 Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
AUTHORS	Santa-Cruz,S., Pogue,G.P., Toth,R.L., Chapman,S. and Carr,F.
TITLE	Expression of foreign genes from plant virus vectors
JOURNAL	Patent: WO 02055719-A 5 18-JUL-2002;
FEATURES	BIOSOURCE GENETICS CORPORATION (US)
Source	Location/Qualifiers
1. 181	
/organism="Potato virus X"	
/mol_type="genomic DNA"	
/db_xref="taxon:12183"	
BASE COUNT	64 a 24 c 49 g 44 t
ORIGIN	
Query Match	96.3%; Score 181; DB 6; Length 181;
Best Local Similarity	100.0%; Pred. No. 6.3e-38;
Matches	181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GTGCAGCGGTATCGAATAAGCTTGATATCGAATTCGTCGATTCGGTTCGACGATTTAAAGCG 60
DB	1 GTGCAGCGGTATCGAATAAGCTTGATATCGAATTCGTCGATTCGGTTCGACGATTTAAAGCG 60
OY	61 GTTGACAACCTTTAAAGAGAGAAAAAGAGGTTGAAGAAAAAGGCTGTAGTAAGTAT 120
DB	61 GTTGACAACCTTTAAAGAGAGAAAAAGAGGTTGAAGAAAAAGGCTGTAGTAAGTAT 120
OY	121 AAGTACAGACCGGAGAGAGTACGCCGCTCGATTCGTTAATTGGAAGAGAAAGAGCT 180
DB	121 AAGTACAGACCGGAGAGAGTACGCCGCTCGATTCGTTAATTGGAAGAGAAAGAGCT 180
OY	181 C 181
DB	181 C 181

RESULT 3

AX511573 181 bp DNA linear PAT 27-SEP-2007

LOCUS AX511573
DEFINITION Sequence 7 from Patent WO02055719.
ACCESSION AX511573
KEYWORDS AX511573.1 GI:23392412

SOURCE
Potato virus X
Tobacco virus X
Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.

REFERENCE
1 Santa-Cruz, S., Pogue, G.P., Torch, R.L., Chapman, S. and Carr, F.
Expression of foreign genes from plant virus vectors
Patent: WO 02055719-A 7.18-Jul-2002;
BIOSOURCE GENETICS CORPORATION (US)
Location/Qualifiers
1..181

FEATURES
source
/organism="Potato virus X"
/mol_type="genomic DNA"
/db_xref="taxon:12183"

BASE COUNT 61 a 28 c 53 g 39 t

ORIGIN

Query Match 87.8%; Score 165; DB 6; Length 181;
Best local similarity 94.5%; Pred. No. 1.2e-33;
Matches 171; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 GTCGACGGTATCATAGCTTGATTGCAATTCGTGCATTCGTTGCGACATTTAAACG 60
| | | | |
Db 1 GTCGACGGTATCATAGCTTGATTGCAATTCGTGCATTCGTTGCGACATTTAAACG 60

OY 61 GTTGACAACCTTTAAAAGAAGAAAAAAGAGTTGAAGAAAAGCGTGTAGTAGTAGTAT 120
| | | | |
Db 61 GTTGACGCCCTTTAAAAGAAGAAAAAAGAGGTTGAAGAAAAGCGGTAGTAGTAGTAT 120

OY 121 AAGTACAGACCAGGAAGTAGCCGGCTCCTGATTGCTTAATTGAAGAAAAGACT 180
| | | | |
Db 121 AAGTACAGACCAGGAAGTAGCCGGCTCCTGATTGCTTAATTGAAGAAAAGAGACT 180

OY 181 c 181
|
Db 181 c 181

RESULT 4

S68164 1537 bp DNA linear VRL 23-SEP-1994

LOCUS S68164
DEFINITION transport protein, capsid protein [tobamovirus; host: cruciferous plants, genomic, 1537 nt].
ACCESSION S68164
VERSION S68164.1 GI:544600

KEYWORDS Tobamovirus
Tobamovirus
viruses; ssRNA positive-strand viruses, no DNA stage.
1 (bases 1 to 1537)

REFERENCE Dordickov, Iu. L., Ivanov, P. A., Novikov, V. K., Yefimov, V. A. and Afabekov, I. G.
AUTHORS Tobamovirus of cruciferous plants: nucleotide sequence of genes of the transport protein, capsid protein, and 3'-terminal untranslated region
Dokl. Akad. Nauk. 332 (4), 518-522 (1993)

TITLE MEDLINE 94083923
PUBMED 8260923
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1dbsg 142918] from the original journal article.
This sequence comes from Fig. 2.
Location/Qualifiers
1..1537
/organism="Tobamovirus"
/mol_type="genomic DNA"
/db_xref="taxon:12234"
103..906

FEATURES
source
gene

[illegible]

```

REFERENCE 3 (bases 1 to 6312)
AUTHORS Dorokhov, Yu. L., Ivanov, P. A., Novikov, V. K., Agranovsky, A. A.,
TITLE Morozov, S. Yu., Efimov, V. A., Casper, R. and Atabekov, J. G.
Complete nucleotide sequence and genome organization of a
JOURNAL tobamovirus infecting cruciferae plants
MEDLINE 94341372
PUBMED 7545946
REFERENCE 4 (bases 1 to 6312)
AUTHORS Belenovich, E., Genetozov, E., Novikov, V. and Zavrlev, S.
TITLE Properties and the genome structure of the K2 strain of tobacco
JOURNAL mosaic virus
REFERENCE 5 (bases 1 to 6312)
AUTHORS Dorokhov, Y.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1994) Dorokhov Y., A. N. Belozersky Institute,
REMARK Moscow State University, Moscow, Russia
FEATURES
    source
        1..6312
            location/qualifiers
    misc_feature
        1..6312
            /organism="Tobacco mosaic virus"
            /mol_type="genomic RNA"
            /db_xref="taxon:12242"
            1..6312
            /note="genomic RNA of the tobacco mosaic virus infecting
            cruciferous plants"
            69..4874
            /function="protein containing RNA-dependant RNA
            polymerase"
            /note="ORF2
            readthrough protein"
            /transl_start=1
            /transl_except="(pos:3390..3392,aa:OTHER)
            /product="178k"
            /protein_id="CA82559.1"
            /db_xref="GI:619908"
            /db_xref="SPTREMBL:Q88604"
            /translation="MAQFOQTIDMOTLOAAAGPNSLVNDLARSRYDNAVELNARSH
            RPVYHSGKASTTEOTLIATNAPPEFISFHTGAVHSLAGFSLLEYLMOVPFEG
            SLVYDGGNSAVLEFKGRDYVHCMPMLDYRDIARHGKHKAHSYVNRKROORPVP
            EYORAFENNYAENDPHYCDKRPCCCLTANGCQRYAVALLSYDIPIVEFGSALLR
            KNYKTCFAFHREHNNLLDCDVTYTLDEIGATFOAGNLSFFHNESTLNTFSNR
            IKVCTKTFEPASQREVTYHKEFLVTRVWTWCKFTFRVDTFLRGVYHNNVDCSEFYR
            VNDMAVYKTKLAMI,NAERTIEKDNALNFWPEPKRDMYIVPLFASITTGMSREYV
            VMDPFTVYLNHKTQYAKALTYANVSPFESISRYVINGVARSMDGDKALIGP
            AMEFLITRKGHODEITILKFOKFORHTNELIWTSLCDALMGVTPKVEKTELVRGQV
            KVAFOLAEIKPIPELCPFADRIYQYKKAEEFOSCDLSKPLESEKTYNNALSELVLE
            NIDSPLEAKRTLCQOKSDVPDMAKAYVAIMKELTLPFKPIPEEISESLKGTGEG
            SASHKDLISLQNDAPPCVKNLVEGSPVAYGMCCKGGGFKLDVIDADFLKSYDAVAK
            RGTGMSAVVYGSIEVRQMKNTIDYLSASLAVSNLCKVLRDVGVQVPESEKSGVMD
            VGRGMLTKLPKNASHAGVAEDANHKYVILGLNMDDEKPCVDEWFNVAASDLSLVS
            DMKLTILTCSPNGEPEBNKARYIIVDYGKLLNDDKPELIEKVSFSDLLIIPKES
            KMIIRRANHGVIRADKDNVSTYDPSLHMSRRNFKPLFIDEGMLTGCYNPLILLS
            OCIVAVYVGTQOIPRICRANPYPYRHPKALVADESEVRVTRTICADVYTFENKRY
            DGVNCTSAVERSVKAEVNRGKALNITLPLEKLTITFQADKFEELLEGKQDVNTV
            MEUQSTFLEKTAIVRLSTPLETISRASPHVLAALTRHTRCXYIVLDPVAVISEE
            HETLSNFLEKTAIVRAGIOXOLOIDAFKSTNLFVOTPKSGDMRDMOFYNDTLPGNS
            TILNEDATVMTNLDISLANKDCRIDSKSVOLPEKQPIFKPIRTAAEMPTAGILL
            ENYVAKIRRMNA.PDLGTGTDIEDTASLVEKRWDSITDKFEGTNNMTYRESFNRW
            LSKQESTYTGQLADNFVVDLPAVDETKHMKISQKQKLDLSIDETPALOTIYHSHK
            IYNSQEPMSFSEVRLTLMLERIDSSKFLFYTKRTPAQIIDEFSDSDSTOAMBLELIDSK
            YKISQEPMSFSEVRLTLMLERIDSSKFLFYTKRTPAQIIDEFSDSDSTOAMBLELIDSK
            VTFEINTTIIIACTLSMIPDKVIKAAFGCDLSLITPGKGLDPTCAOANLMMNPE
            AAFKFKYGFEGGRVYIHDRGALIVYDPLKLSITGCKRIIRGVHVEELRESLCDVA
            SNLNAAVPSQDDEAAVAEHKTRAVGGSFACSTIIKLSDRKLRLDLEFV"
        69..3392
            /function="protein containing methyltransferase &
            RNA-helicase domains"
            /note="ORF1"
            /codon_start=1
            /product="122k"
            /protein_id="CA82558.1"

```

```

/db_xref="GI:488714"
/db_xref="SPTREMBL:Q88603"
/translation="NAQFOQIDMOTLQAAGPNSLVNDLASRRVYDNAVEELNRSR
RKHVHRSKAVSTEQTLIATNAPFEFISTHTQSAVSHSLAGFSRLELEYLMAQVFG
SLYDIGNFSAHLFKRDYVHSCAMPNLDVRIARHEGKCAHSHSVNKLKQOHPV
EJORAFAFNYPANPHFBDKDPDOCELTAGTPTVYALALSTIDPIEEGSAIIR
KVKQCFAPAFHEHNNMLDDCVTLDELGATQORAGDNLSFFPHNSTLNTYHSNII
IKYCKTPPAPQRFYHKEFLVTVNNTVCFTVVDVFTFLRGVYHNNVDEEYKA
KDDAMHKKTKTLMLNAERTIFEDNALAMFWFKVNDVLPDASITGRSREVM
VAKDFVYVYLNHIKTYQAKALYANVLSVESISRVIIVTARSEMOTDAIIGPL
NATFLIKGLHGVDEILKFKQEDRTNELITSLCALMGVISPSEKTELVRGFG
KYABOALEIKIPELCTFADRLVLYKKAEHOSGDISPLESEKRYNALSELVLE
NIDSPDLAPKTLCOOKSVDPDMAKVVYAIKRCCLLPKPTPEEISESTGEAT
SAEHKDVSLQNDAPPCYKKNVESVRAIGCPGGGDKLDVADIADHLKSVDAVK
RGTMSAVYTGSIYVRQMKNTIDYLSASLSATVSNLCVLRDVGVDPEOSDKSVWD
VARGKMLKTPNKSIAHGVADANHLIYVLNMDGKRVCDDETFRVAVSSDLSIYS
DMGKLTITLTCSPNEPEPEPNKAVILVDVPGCGKTEIEKVFSEDLIYVGEAS
KMIIRANAGVIRADKDNVSTVDSFLMHPSRVRKLEIDEGMLHGVCELLLS
OCDVAVYVDQIOIPICRVANFPYPAHAKVADKEKRRRTYRCPADMYELKKY
DGAVMCTSAVERSVKAEVYRGALNPITPLEGILITPTQADKELLEKTKVDNIV
HEVQETYEKTAIVLITSTPLETISRASPHVLAITRHTTCKYITVLDPMVNISE
MEKLSNFLDMTRVEAGIQ"
/feature="transport protein"
/function="ORF3"
/codon_start=1
/product="29k"
/protein_id="CAA82560.1"
/db_xref="GI:488715"
/db_xref="SPTREMBL:Q88605"
/translation="MSIYSEPKVSDPFLNLSKKEILLPKALTRKTVSISKTDIISV
ESNLCIDILINPLDKRYVGLIIGAVFTGEMLYPDDKGVSTISVDKLANKEC
VIGTRAAKSKRFQKLPNTFVSTVAKRPMQVHRIODKLTAEMKRRKKVYEV
VAAVTNNVVMGLREKVVAAINDPVEGEGVDFVDAFAKADNFKRRKKVEEK
GVSKYKRPKRIAGPDSFNLKEENVLOHYRESVYPERSGVRAHSDA"
5604..6077
/function="coat protein"
/note="ORF4"
/codon_start=1
/product="18k"
/protein_id="CAA82561.1"
/db_xref="GI:488716"
/db_xref="SPTREMBL:Q88606"
/translation="MSYNTINPOXYOAAVMAAPRIPMLNOCISLSSSYTOAARD
VROQFSNLSAVAPASQRFPTSGSRVYNSVIRPLALKSEPTNRRIITEESR
PSASEVRNATQVRDQATVSIHQIQLLSELSSGGMNRAFEFALVETWTAAT"
BASE COUNT      1800 a      1213 c      1590 g      1709 t
ORIGIN
Query Match      83.7%; Score 157.4; DB 14; Length 6312;
Best Local Similarity 93.7%; Pred. No. 1.3e-31;
Matches 164; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 GTCGACGGTATCGATAGCTGATATCGATTCGATTCGGTTCGACGATTTAAACG 60
|||||
DB 5429 GTCGAAGGTTTCGAAGGTGTGATGACGATTCGATTCGGTTCGACGATTTAAACG 5488
|||||

OY 61 GTTGCAACTTTAAAGAGAAAAGAGAGTTGAAGAAAAGGTTAGTAAGTAAGTAT 120
|||||
DB 5489 GTTGCAACTTTAAAGAGAAAAGAGAGTTGAAGAAAAGGTTAGTAAGTAAGTAT 5548
|||||

OY 121 AAGTACAGACGGGAGAGTACGGCGGTCGATTCGTTATTTGAAAGAGAA 175
|||||
DB 5549 AAGTACAGACGGGAGAGTACGGCGGTCGATTCGTTATTTGAAAGAGAA 5603
|||||

RESULT 6
AX511572      180 bp      DNA      linear      PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 6 from Patent WO02055719.
ACCESSION AX511572
VERSION AX511572.1 GI:23392411
KEYWORDS

```

```

SOURCE
ORGANISM      Potato virus X
REFERENCE
AUTHORS      Santa-Cruz, S., Pogue, G.P., Toth, R.L., Chapman, S. and Carr, F.
TITLE        Expression of foreign genes from plant virus vectors
JOURNAL
JOURNAL
BIOSOURCE    GENETICS CORPORATION (US)
FEATURES
source
1..180
/organism="Potato virus X"
/mol_type="genomic DNA"
/db_xref="taxon:12183"
BASE COUNT      60 a      31 c      52 g      37 t
ORIGIN
Query Match      80.5%; Score 151.4; DB 6; Length 180;
Best Local Similarity 93.4%; Pred. No. 5.1e-30;
Matches 169; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

OY 1 GTCGACGGTATCGATAGCTGATATCGAATTCGTCGATTCGGTTCACGATTTAAACG 60
|||||
DB 1 GTCGACGGTATCGATAGCTGATATCGAATTCGTCGATTCGGTTCACGATTTAAACG 59
|||||

OY 61 GTTGCAACTTTAAAGAGAAAAGAGAGTTGAAGAAAAGGTTAGTAAGTAAGTAT 120
|||||
DB 60 GCTGACAAACCCCTAAAGAGAAAAGAGAGTTGAAGAAAAGGTTAGTAAGTAAGTAT 119
|||||

OY 121 AAGTACAGACGGGAGAGTACGGCGGTCGTCGATTCGTTAATTTGAAAAGAGAGCT 180
|||||
DB 120 AAGTACAGACGGGAGAGTACGGCGGTCGTCGATTCGTTAATTTGAAAAGAGAGCT 179
|||||

OY 181 c 181
DB 180 c 180

RESULT 7
AX511569/c
LOCUS
DEFINITION Sequence 3 from Patent WO02055719.
ACCESSION AX511569
VERSION AX511569.1 GI:23392408
KEYWORDS
SOURCE
ORGANISM      Potato virus X
SOURCE
Potato virus X
Potato virus X
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
REFERENCE
1
AUTHORS      Santa-Cruz, S., Pogue, G.P., Toth, R.L., Chapman, S. and Carr, F.
TITLE        Expression of foreign genes from plant virus vectors
JOURNAL
JOURNAL
BIOSOURCE    GENETICS CORPORATION (US)
FEATURES
source
1..187
/organism="Potato virus X"
/mol_type="genomic DNA"
/db_xref="taxon:12183"
BASE COUNT      45 a      47 c      27 g      68 t
ORIGIN
Query Match      79.8%; Score 150; DB 6; Length 187;
Best Local Similarity 96.8%; Pred. No. 1.2e-29;
Matches 153; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 29 AATCGTCGATTCGGTTCACGATTTAAAGGGTGAACAAGCTTTAAAGAGAGAAAAGA 88
|||||
DB 180 AATCGTCGATTCGGTTCACGATTTAAAGGGTGAACAAGCTTTAAAGAGAGAAAAGA 121
|||||

OY 89 AGGTTGAAGAAAAGGTTAGTAAGTAAGTAAGTACAGACCGAGAGTACCGCGGTC 148
|||||
DB 120 AGGTTGAAGAAAAGGTTAGTAAGTAAGTAAGTACAGACCGAGAGTACCGCGGTC 61
|||||

OY 149 CTGATTCGTTAATTTGAAAGAGAGAGCTCACCAT 186

```

Db 60 CTGATTCGTTTAAATTGAAGAGAAAGATTGCATAT 23

RESULT 8
AX511568

LOCUS AX511568 251 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 2 from Patent WO02055719.

ACCESSION AX511568

VERSION AX511568.1 GI:23392407

KEYWORDS

SOURCE Potato virus X

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.

REFERENCE 1
Santa-Cruz, S., Pogue, G. P., Toth, R. L., Chapman, S. and Carr, F.
Expression of foreign genes from plant virus vectors
JOURNML PATENT: WO 02055719-A 2 18-JUL-2002;
BIOSOURCE GENETICS CORPORATION (US)

FEATURES
source
1..251
/organism="Potato virus X"
/mol_type="genomic DNA"
/db_xref="taxon:12183"

BASE COUNT 72 a 51 c 76 g 52 t

ORIGIN

Query Match 79.3%; Score 149; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.2e-29;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CGAATTCGTCGATTCGCTTGACGATTTAAAGCGGTTGACAACTTTAAAGAGAAAA 86
|||||
Db 97 CGAATTCGTCGATTCGCTTGACGATTTAAAGCGGTTGACAACTTTAAAGAGAAAA 156
|||||

QY 87 GAAGCTGAGAGAAAAAGGCTAGTAGTACGTATAGTACAGAGCCGGAAGTACGCCGG 146
157 GAAGCTGAGAGAAAAAGGCTAGTAGTACGTATAGTACAGAGCCGGAAGTACGCCGG 216
|||||

QY 147 TCCGATTCGTTTAAATTGAAGAGAAAA 175
|||||
Db 217 TCCGATTCGTTTAAATTGAAGAGAAAA 245
|||||

RESULT 9
BRU03387

LOCUS BRU03387 6311 bp RNA linear VRL 18-FEB-1998

DEFINITION Turnip vein-clearing virus, complete genome.

ACCESSION U03387.1 GI:2894629

VERSION U03387.1 GI:2894629

KEYWORDS

SOURCE Turnip vein-clearing virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.

REFERENCE 1
Larter, R. T., Lane, L. C. and Melcher, U. K.
Electron microscopic and molecular characterization of turnip
vein-clearing virus
JOURNML Arch. Virol. 138 (3-4), 287-298 (1994)

MEDLINE 95091521

PUBMED 7998835

REFERENCE 2
Larter, R. T., Voss, T. C. and Melcher, U. K.
Completion of a cDNA sequence from a tobamovirus pathogenic to
crucifers
JOURNML Gene 166, 321-322 (1995)

REFERENCE 3
Melcher, U. K.
Direct Submission
JOURNML Submitted (09-NOV-1993) Biochemistry & Molecular Biology, Oklahoma
State University, NRC 246, Stillwater, OK 74078-0454, USA
4 (pages 1 to 6311)
Melcher, U. K.

TITLE Direct Submission

JOURNAL Submitted (18-FEB-1998) Biochemistry & Molecular Biology, Oklahoma
State University, NRC 246, Stillwater, OK 74078-0454, USA

REMARK Sequence update by submitter

COMMENT On Feb 18, 1998 this sequence version replaced gi:619581.

FEATURES
source
1..6311
/organism="turnip vein-clearing virus"
/mol_type="genomic RNA"
/strain="OSU"
/specific_host="Brassica rapa"
/db_xref="taxon:29272"
/lab_host="Nicotiana tabacum"
/note="possibly an isolate of ribgrass mosaic virus"
68..4873
/note="contains RNA polymerase; stop codon at 3389..3391
is suppressed under certain conditions and expressed as
tyrosine"
/codon_start=1
/transl_except="(pos:3389..3391,aa:Tyr)
/product="RNA replicase read-through component"
/protein_id="AAC02783.1"
/db_xref="GI:619645"
/translation="MAQFOQTIDMOTLQAAGRNLSVNDLASRRVYDNAVEELNARSR
RPKVFHRAVSTEOITLATNAYPEFEISFTQSVAHSLAGLSLELEYLMQVPCG
SLTYDIGNFSAHLEKGRDHYVCCMPNDVIDIARHGHKRAIYSVNRILRQORPVP
EYORAPFNNAENPFIHCDKPRQOCETITATGDTTAYALHSITDIVEERGSALR
KNVCTCFAPFHEHMLDCTVLDLGATFQKSGDNLSEFFHNESTLNTSHSNI
IRYCKTFEPASQFVHRELFVNVNMYCKTFEVDVFTLEFRGYHNNVCEERYKA
MDDAWHYKRTLAMNAERTIFDNALNEMFPKVDNVIYPLDASITGMRREIM
VNKDEVYVUNHKTGYOAKALTYANVLSFVSIISRYINGVTAASEMDPKAITGLP
AMTEFLIRKIGHVODEITLKKRQEDRTNELISGLDAMGVIPSKETLYNGFP
KYABALRIKPELCTETADRLVIQYKAEEROSDLSKPLESEKRTINALSELSLE
NDSFDLEAFETLCOQKNDVPMKAVVNAKLSLTLFPRKPEEELISELKPQEGS
CAEHKEVLSLQNDAPFCVKNLVESGVAYGCGGFGFLDVIDIDFHLKSDAVK
KGTWMSAVYTSQIDKQKNTIDYLSASLAVSNLCKVLBDVHGVDSESGQVW
VRGRWMLKPNKSHAGVADANHLIYVLNMDQKPCVODETFRVAVSDELITS
DMGRTKTLTSCSPNGEPPEPNKAVILVGVGCGCTKEITIKVESDILIPKREAS
KMIIRANQAVYTRADKRNRYVDSFLMHSRPRFKRLFTDEGLMLHGCNVLILLS
QCDVAVYGDTRQIDPEICRVNFPYPAHFALVDEKVRNVTILRCPELADVIYFLNKY
DGAVNCYSVABRVAEYVGRGALNPITPLEGILFETQADKFLDEKQIKVNTV
HEVOGETYKTAIVALTSTPLEIISAPHLVLAIRTTCCRYTVVLYDENVYVISE
MEKLSNFFLDNMYRVAGVOYOLIDAVRDSNLVFOQPKSGDMGVYDVALPQNS
TILNEFDVATNINDISLNVDCRDRDSQVLPQEQIPLKPKRTTAAEPFRAGIL
ENLYAMIKRNMAPDLTGITIDEDTASLVKRFNDVYDKESFGNETMTRESFRR
LSKQESSVQLADPNFVDLPVADYEYKIMNISQPKLIDLSIODEYPALQIYVHSK
INAIFFGPFSELTATLRLERIDSKEFLFTRTPQAOIEPFSDLDSTQAMELIEDISK
YDKSONEHCACAVKIMKELGIDEMIAVMOGHRKTLTKDYGAVKTCIMYORKSGD
VTTFPGNTIITIAAGLSSMIPMDKVIKAFCGDDSLIYPRGLDLPIDQAGANLWNP
AKIFRRKYVCGRGIYVHHDGAIYVYPLKISLKGKHTRDVYHLEELRESLCDVA
SNLNCATFSOLDENAVAEHKTAVGGSFAFSIITKYSKRLFDLFPV"
68..3391
/note="contains capping methyltransferase and RNA helicase
domains"
/codon_start=1
/product="RNA replicase component"
/protein_id="AAC02782.1"
/db_xref="GI:514836"
/translation="MAQFOQTIDMOTLQAAGRNLSVNDLASRRVYDNAVEELNARSR
RPKVFHRAVSTEOITLATNAYPEFEISFTQSVAHSLAGLSLELEYLMQVPCG
SLTYDIGNFSAHLEKGRDHYVCCMPNDVIDIARHGHKRAIYSVNRILRQORPVP
EYORAPFNNAENPFIHCDKPRQOCETITATGDTTAYALHSITDIVEERGSALR
KNVCTCFAPFHEHMLDCTVLDLGATFQKSGDNLSEFFHNESTLNTSHSNI
IRYCKTFEPASQFVHRELFVNVNMYCKTFEVDVFTLEFRGYHNNVCEERYKA
MDDAWHYKRTLAMNAERTIFDNALNEMFPKVDNVIYPLDASITGMRREIM
VNKDEVYVUNHKTGYOAKALTYANVLSFVSIISRYINGVTAASEMDPKAITGLP
AMTEFLIRKIGHVODEITLKKRQEDRTNELISGLDAMGVIPSKETLYNGFP
KYABALRIKPELCTETADRLVIQYKAEEROSDLSKPLESEKRTINALSELSLE
NDSFDLEAFETLCOQKNDVPMKAVVNAKLSLTLFPRKPEEELISELKPQEGS
CAEHKEVLSLQNDAPFCVKNLVESGVAYGCGGFGFLDVIDIDFHLKSDAVK
KGTWMSAVYTSQIDKQKNTIDYLSASLAVSNLCKVLBDVHGVDSESGQVW
VRGRWMLKPNKSHAGVADANHLIYVLNMDQKPCVODETFRVAVSDELITS
DMGRTKTLTSCSPNGEPPEPNKAVILVGVGCGCTKEITIKVESDILIPKREAS
KMIIRANQAVYTRADKRNRYVDSFLMHSRPRFKRLFTDEGLMLHGCNVLILLS
QCDVAVYGDTRQIDPEICRVNFPYPAHFALVDEKVRNVTILRCPELADVIYFLNKY
DGAVNCYSVABRVAEYVGRGALNPITPLEGILFETQADKFLDEKQIKVNTV
HEVOGETYKTAIVALTSTPLEIISAPHLVLAIRTTCCRYTVVLYDENVYVISE
MEKLSNFFLDNMYRVAGVOYOLIDAVRDSNLVFOQPKSGDMGVYDVALPQNS
TILNEFDVATNINDISLNVDCRDRDSQVLPQEQIPLKPKRTTAAEPFRAGIL
ENLYAMIKRNMAPDLTGITIDEDTASLVKRFNDVYDKESFGNETMTRESFRR
LSKQESSVQLADPNFVDLPVADYEYKIMNISQPKLIDLSIODEYPALQIYVHSK
INAIFFGPFSELTATLRLERIDSKEFLFTRTPQAOIEPFSDLDSTQAMELIEDISK
YDKSONEHCACAVKIMKELGIDEMIAVMOGHRKTLTKDYGAVKTCIMYORKSGD
VTTFPGNTIITIAAGLSSMIPMDKVIKAFCGDDSLIYPRGLDLPIDQAGANLWNP
AKIFRRKYVCGRGIYVHHDGAIYVYPLKISLKGKHTRDVYHLEELRESLCDVA
SNLNCATFSOLDENAVAEHKTAVGGSFAFSIITKYSKRLFDLFPV"

	MSAYTQKINQOKNMFVDYASLSTLSAVSNICLYRLDVGHVDESGOEKSGMPVYBRR RMLLKPNARKHANGVAENBAENKRLITVLIMMDGKPYCDQFMYRLAIVSDSLIYSDMR LKLTISCCVDBEPEPRKAKVYLVDGVBCCGTKTEILEVNSSEDLVPYGKAESKMTII IRAMQDTRADRONRVATDSFLHPHPRKVRKRLFIDGLMHTGCYNFTLIISQCID AYAGVDFQOIPFICRVANEPYPKHFAHLYVDEKDRITLLCPADYVIFELKKKYDGSA LCSTSSERSVSAAOVVRKGALNPITLLPLEGILTFETQADKFELDCKGYDVNTVHEVO GETENKTAVLRITAPLETLIISRAPHVLAHLRTHTSCKYPTVLDPLVVISIMEKTI SNFIIDMKVBSGng"
CDS	4865..5665 /codon_start=1 /product="movement protein" /protein_id="BAB82446.1" /db_xref="GI:18146772" /translation="MSTSYSKPKYSDFLTLSRTEEILPKALTRLKTVSVSRKDVIYWK ESESCLDILLVNPIDLKFRVYGLIGVAFGEMLIPRYNGGVYVSVIDRLEMSKECI IIGTYRAARDNRQFKLVPIFYTSYDADEKARPMQVHRRIIONKLIEGMQDLAEVVS VAANTNNVVAKGLERERYIAVDDPVESEGVDVFIDSVAFAKVDFRKKKRIGGR DIVIKRYRPREKRYKVGPSLLNKNEENVIOHHELSEVPYFRSGMGGAHSNA" 5589..6062 /codon_start=1 /product="coat protein" /protein_id="BAB82447.1" /db_xref="GI:18146772" /translation="MSYNIINSNQYOFEFAVMABEIAMLNOCVSALSOSYOTOGAADPT VROQFSNLTAIYTPNORPETGGRYVNSAVLKLVELALKMSPDTRNRIETEESER PSASEVNAAIQRVDDAVAIRSOITOLLSELSSHGLMNRAEEFVLLIPMAFPARK"
BASE COUNT	1807 a 1147 c 1591 g 1752 t
ORIGIN	
Query Match	63.3%; Score 119; DB 14; Length 6297;
Best Local Similarity	80.0%; Pred. No. 2,36-21;
Matches 140;	Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Oy	1 GTGCAGCGTTACGTAAAGCTTGATATGGAATTCCTCATTCGTTGCAACATTAAAGCG 60 Db 5414 GTTAGAGGTTTCAGAGGTGTGAGCAGCAATTCATTCGTTGCAACATTAAAGCG 5473
Oy	61 GTTGACAACCTTTAAAGAAGAAAAAGAAGGTGMAAAAAGCGGTGTAAGTAAGTAT 120 Db 5474 GTTGACAATTTTCAGCAAAAAAGAAAAAGAAGTTGCAAGAGGAGATGTGATTAGAAATAT 5533
Oy	121 AAGTCAGACCCGGAAGACTACGCCGGTCCGTGATTCGTTTATTTGAAGAAGAAA 175 Db 5534 AAGTATGACCAGAGAAGTACGCCGGTCCGTGATTCGTTTATTAATAAAGAAGAAA 5588
RESULT 12	
AB017503	
LOCUS	6298 bp RNA linear VRL 14-FEB-2002
DEFINITION	Crucifer tobamovirus genomic RNA, complete genome,
LOCATION	Isolate:shizuoka.
ACCESSION	AB017503
VERSION	AB017503.1 GI:18146763
KEYWORDS	
SOURCE	Crucifer tobamovirus
ORGANISM	Crucifer tobamovirus
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
AUTHORS	Lee,K., Nishiguchi,M. and Kashiwazaki,S.
TITLE	Complete nucleotide sequences of two isolates of crucifer tobamovirus unpublished
JOURNAL	2 (bases 1 to 6298)
REFERENCE	Lee,K., Nishiguchi,M. and Kashiwazaki,S. Direct Submission Submitted (07-SEP-1998) Satoshi Kashiwazaki, National Agriculture Research Center, Department of Plant Protection; 3-1-1 Kannondai, Tsukuba, Ibaraki 305-8666, Japan (E-mail:skashiwa@narc.affrc.go.jp, Tel:81-298-38-8932, Fax:81-298-38-8925)
FEATURES	Location/Qualifiers 1..6298 /organism="Crucifer tobamovirus" /mol_type="genomic RNA"

1	188	100.0	188	24	ABO76058	Clone TYS-GFP-IRE
2	181	96.3	181	24	ABO76062	Clone TYS-GFP-IRE
3	165	87.8	181	24	ABO76064	Clone SC197 contra
4	151.4	80.5	180	24	ABO76060	Clone SC196 contra
5	150	79.8	187	24	ABO76053	Clone TYS-GFP-SER
6	149	79.3	251	24	ABO76055	Clone TYS-GFP-HIR
7	148	78.7	148	25	AB257802	Crucifer tobacco r
8	148	78.7	148	25	AB275164	Crucifer tobacco r

IRBS element IRBS
RibPras mosaic v
PBSWT2 vector con
Phlaed transformac
PHK5 vector contri
Plastid transform
Human secreted pr
Human secreted pr
Arabidopsis thalli
Arabidopsis thalli
Tumour suppressor
Arabidopsis thalli
Hormone-like prot
Accessory factor 7
Plasmid pPK9/10 D
Human secreted pro
Arabidopsis thalli
Human secreted pro
Arabidopsis thalli
Human secreted pro
Human secreted pro
Mouse azoospermia
Human prostate exp
Human prostate exp
Human secreted pro
S. aureus MUF ORF
Gibberellin-20-ox
Transformation vec
Human prostate exp
Human secreted pr
Human prostate exp
Human prostate exp
Human secreted pro
Preliminary CLASP
Preliminary CLASP

ALIGNMENTS

RESULT 1	ID	ABQ76058	ABQ76058 standard; DNA; 188 BP.
XX	AC	ABQ76058;	
XX	30-SEP-2002	(first entry)	
DE	Clone	TXS.GFP-IRESs-CP	containing IRES DNA sequence.
XX	IRES;	internal ribosome entry site;	viral protein; bic
KW	virus	infection; coat protein;	protein replacement the
KW	nutritional	value; seed oil content;	ds.
XX	Synthetic.		
OS	W0200255719-A2.		
PN	18-JUL-2002.		
XX	09-JAN-2002;	2002WO-US01123.	
XX	09-JAN-2001;	2001US-0758962.	
XX	(BIOS-)	BIOSOURCE GENETICS CORP.	
PA	Santa-Cruz S,	Pogue GP,	Toth RL,
PI	Chapman S,	Carr F.	
XX	WPI;	2002-557829/59.	
XX	New polypeptides	contained in plant	virus expression vec

PT expression tools, in protein replacement therapy or for intervening in
PT a metabolic pathway to improve the nutritional value of a crop or alter
PT the oil content of seeds -

Claim 4; Fig 3; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading frame (ORF) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant potatovirus X-based viral vector containing a nucleic acid construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosome entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS:GFP-IRES-CP containing an IRES region described in the method of the invention.

SQ Sequence 188 BP; 66 A; 26 C; 51 G; 45 T; 0 other;

Query Match	100.0%	Score 188;	DB 24;	Length 188;
Best Local Similarity	100.0%;	Pred. No. 7,7e-44;		
Matches 188; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	GTCTGACGGTATCTGATTAACCTTGATATGCAATTGCTGCATTCGGTTGCGACATTTAAAGCG	60
Db	1	GTCTGACGGTATCTGATTAACCTTGATATGCAATTGCTGCATTCGGTTGCGACATTTAAAGCG	60
QY	61	GTTCGACACTTTAAAGAAAGAAAAAGAGGTTGAAGAAAAAGGTTAGTAACTAAGTAT	120
Db	61	GTTCGACACTTTAAAGAAAGAAAAAGAGGTTGAAGAAAAAGGTTAGTAACTAAGTAT	120
QY	121	AAATGACAGACCGGAGAAAGTACCGCGGTCTCGATTCGTTAATTGAAAGAAAGAAAGCT	180
Db	121	AAATGACAGACCGGAGAAAGTACCGCGGTCTCGATTCGTTAATTGAAAGAAAGAAAGCT	180
QY	181	CACCATGG	188
Db	181	CACCATGG	188

RESULT 2
ABO76062

ID	ABQ76062	standard; DNA; 181 BP.
----	----------	------------------------

AC ABQ76062;

DT 30-SEP-2002 (first entry)

DE Clone TXS.GFP-IRES-CP containing IREScp DNA sequence.

KM IRES; internal ribosome entry site; viral protein; bicistronic;
 KM virus infection; coat protein; protein replacement therapy; crop;
 KM nutritional value; seed oil content; ds.

OS Synthetic.

PN .W0200255719-A2.

PD 18-JUL-2002.

PF 09-JAN-2002; 2002WO-US01123.

PR 09-JAN-2001; 2001US-0758962.

PA (BIOS-) BIOSOURCE GENETICS CORP.

PI Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F;

DR WPI; 2002-557829/59.

PT New polypeptides contained in plant virus expression vectors, as gene
PT expression tools, in protein replacement therapy or for intervening in
PT a metabolic pathway to improve the nutritional value of a crop or alter
PT the oil content of seeds -

PS Claim 4; Fig 4; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant potex virus X-based viral vector containing a nucleic acid construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosome entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TYS.GFP.IRES-CP containing an IRESCP region described in the invention.

SQ Sequence 181 BP; 64 A; 24 C; 49 G; 44 T; 0 other;

Query Match	96.3%	Score 181;	DB 24;	Length 181;
Best Local Similarity	100.0%	Pred. No. 7.3e-42;		
Matches 181; Conservative	0;	Mismatches	0;	Indels
		Gaps	0	

QY	1	GTCGACGCGTATCGATTAAGCTTGATATCGAATTCGTGATTCGGTTGCAGCAATTTAAAGCG	60
Db	1	GTCACGCGTATCGATTAAGCTTGATATCGAATTCGTGATTCGGTTGCAGCAATTTAAAGCG	60
QY	61	GTTGACCACTTTAAAGAAAGAAAAAGAAAGGTTGAAGAAAGCGGTACTAGTAGACTT	120
Db	61	GTTGACCACTTTAAAGAAAGAAAAAGAAAGGTTGAAGAAAGCGGTACTAGTAGACTT	120
QY	121	AAGTACAGACCGGAGAAAGTACGCGCGTCTGATTTGTTAAATTTGAAAGAAAGAGAGCT	180
Db	121	AAGTACAGACCGGAGAAAGTACGCGCGTCTGATTTGTTAAATTTGAAAGAAAGAGAGCT	180
QY	181	C 181	
Db	181	C 181	

RESULT 3
ABO76064

ID ABQ76064 standard; DNA; 181 BP.

AC ABQ76064;

DT 30-SEP-2002 (first entry)

DE Clone SC197 containing IREScp DNA sequence.

KW IRBS: internal ribosome entry site; viral protein; bicistronic;
KW virus infection; coat protein; protein replacement therapy; crop;
KW nutritional value; seed oil content; ds.

OS Synthetic.

PN WO200255719-A2.

Claim 4; Fig 4; 33pp; English.

Sequence 181 BP; 61 A; 28 C; 53 G; 39 T; 0 other;

1 GTCACGGTATCGAATGATATCGAATTCGTCGATTCGGTTCAGCATTAAAGCG 60

1 GTCGACGGTATCGATTAGCTTGATATCGAATTCGTCGATTCGGCTGCAGCATTAAAGCG 60

[illegible]

101 AAAAAAAAAAAAAAAAAAAAAA

121 AAGTACAGACCGAGAGCAGCGGTCCTGATACGTTAATTGCAACACGACACGCGC 180

181 C 181

181 C 181

T 4

ABQ76063 standard; DNA; 180 BP.

ABQ/6063;

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

05 Synthetic
yy

FN
XX

XX

XX
DP 09-TAN-2001, 2001HC-07E9063

PA (BIOS-) BIOSOURCE GENETICS CORP.

PI Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F, ...

DK WP1; 2002-557829/59.
XX

PS Claim 4; Fig 4; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES), nucleotide sequence, an open reading frame (ORF) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant potatovirus X-based viral vector containing a nucleic acid construct comprising a dicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosome entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone SC196 containing an IRES region described in the method of the invention.

SQ Sequence 180 BP; 60 A; 31 C; 52 G; 37 T; 0 other;

```

Very match      80.36;  score 151.4;  DB 24;  Length 180;
Best Local Similarity 93.48;  Pred. NO. 1 Re-33;

```

[illegible][illegible]

61 GTTGACACTTTAAAGAGGAAAGAGCGTTGAAGAAAAGCGTCTAGTAAGTAAGTAT 120

Db 60 GCTGACAACCTAAAGAAGGAAAAGAGGGTTGAAGAAAGGGTCTAGTAAGTAT 119

121 AAGTACAGACCGGAGAGTACGCCGGTCTGATTCTTAAATTGAAAGAGAAGAGCT 180

[illegible]

—

ABQ76060/c

[illegible]

XX	AB076059 standard; DNA; 251 BP.
XX	AB076059;
XX	30-SEP-2002 (first entry)
XX	Clone TXS.GFP-HIRES-CP containing IRES DNA sequence.
XX	IRES; internal ribosome entry site; viral protein; bicistronic;
XX	virus infection; coat protein; protein replacement therapy; crop;
XX	nutritional value; seed oil content; ds.
XX	Synthetic.
XX	WO200255719-A2.
XX	18-JUL-2002.
XX	09-JAN-2002; 2002W0-US01123.
XX	09-JAN-2001; 2001US-0758962.
XX	(BIOS-) BIOSOURCE GENETICS CORP.
XX	Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F;
XX	WPI; 2002-557829/59.
XX	New polypeptides contained in plant virus expression vectors, as gene
XX	expression tools, in protein replacement therapy or for intervening in
XX	a metabolic pathway to improve the nutritional value of a crop or alter
XX	the oil content of seeds
XX	Claim 4; Fig 3; 33pp; English.
XX	This invention describes a novel isolated polynucleotide comprising an
XX	internal ribosome entry site (IRES) nucleotide sequence, an open reading
XX	frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein,
XX	where the IRES is located between ORF1 and ORF2. The novel
XX	polynucleotides of the invention are used in the construction of a
XX	recombinant potato virus X-based viral vector containing a nucleic acid
XX	construct comprising a bicistronic message with an intervening IRES. The
XX	constructs are used in a method for regulating the rate at which a virus
XX	infection spreads in a host. Regulation is achieved by placing the
XX	nucleic acid construct comprising an internal ribosome entry site
XX	upstream of a coat protein gene, where the IRES is chosen by the rate of
XX	infection of the viral vector on a host in the presence of that IRES. The
XX	polynucleotide and vectors of the invention are useful for directing
XX	rapid and high-level expression of foreign genes in mature,
XX	differentiated, plant tissue. These are particularly useful in protein
XX	replacement therapy, or for intervening in a metabolic pathway to improve
XX	the nutritional value of a crop or alter the oil content of the seed.
XX	This sequence represents a fragment of the clone TXS.GFP.HIRES-CP
XX	containing an IRES region described in the method of the invention.
XX	Sequence 251 BP; 72 A; 51 C; 76 G; 52 T; 0 other:
XX	Query Match 79.3%; Score 149; DB 24; Length 251;
XX	Best Local Similarity 100.0%; Pred. No. 9.1e-33;
XX	Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	27 CGAATTCGTCATTTCGGTTGCAAGCACTTTAAAGCGGTGACAACTTTAAAGAAGAAAA 86
DB	
DB	97 CGAATTCGTCATTTCGGTTGCAAGCACTTTAAAGCGGTGACAACTTTAAAGAAGAAAA 156
QY	87 GAAGCTGAAGAAAAAGGCTAGTAGTAAGTAAGATAAGTACAGACCGGAGAACTAGCCGG 146
DB	
DB	157 GAAGCTGAAGAAAAAGGCTAGTAGTAAGTAAGATAAGTACAGACCGGAGAACTAGCCGG 216
QY	147 TCCTGATTCGTTTAATTTGAAAGAAGAA 175
DB	

Db 217 TCCTGATTCGTTAATTGAAAGAGAAA 245

RESULT 7

ID AB257802 standard; DNA; 148 BP.

AC AB257802;

DT 07-APR-2003 (first entry)

XX Crucifer tobacco virus internal ribosome entry site IREScp148.

XX Internal ribosome entry site; IRES; transgenic plant; ss.

OS Crucifer tobacco mosaic virus.

PN WO2002101006-A2.

PD 19-DEC-2002.

PF 07-JUN-2002; 2002WO-US17927.

PR 08-JUN-2001; 2001US-297103P.

PA (ICON-) ICON GENETICS INC.

PI Hall G, Bascomb N, Bossie M;

PI WPI; 2003-167400/16.

PT New nucleic acid constructs comprising a transcriptional regulatory element, first and second coding regions, and an internal ribosome entry site element, useful for transiently or stably expressing active biomolecules in plants

PT Disclosure; Page 10; 40pp; English.

XX The present sequence is the nucleotide sequence of internal ribosome entry site IREScp148cr from the genome of the crucifer tobacco mosaic virus. The invention relates to the production of complex proteins in plants. Nucleic acid constructs contain, from 5' to 3', a transcription initiator and a plurality of structural genes, each separated by an IRES. In a claimed nucleic acid construct, the IRES is IREScp148. Complex proteins that in their native state require the coordinate expression of several genes to become biologically active can be produced. The products typically possess therapeutic, diagnostic or industrial utility, and include an antibody, especially a monoclonal antibody, which may be human or humanised, or preproinsulin (expressed with a processing protein to convert the inactive protein to active form), and may also be a T cell receptor, an MHC protein, a protein of the immunoglobulin superfamily, interferon, interleukin, a hormone, an antigen, a receptor, a nucleic acid binding protein, an abzyme, a growth factor, a cell membrane protein, a differentiation factor, a haemoglobin-like protein or a multimeric kinase (claimed). The plant may be Arabidopsis, Brassica, maize, alfalfa, soybean, tobacco, crucifera, cottonseed, sunflower or a legume.

XX Sequence 148 BP; 56 A; 17 C; 40 G; 35 T; 0 other;

Query Match 78.7%; Score 148; DB 25; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.5e-32; Mismatches 0; Indels 0; Gaps 0;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 GAATTCGTCGATTCGTCGACATTAAAGCGGTGACACTTTAAAGAGGAAAAAG 87
 DB 1 GAATTCGTCGATTCGTCGACATTAAAGCGGTGACACTTTAAAGAGGAAAAAG 60
 OY 88 AAGTTGAAGAAAGGCTGTAGTAAGTATTAAGTACAGACCGAGAAAGTACCCGGT 147
 DB 61 AAGTTGAAGAAAGGCTGTAGTAAGTATTAAGTACAGACCGAGAAAGTACCCGGT 120

OY 148 CCGTATTCGTTAATTGAAAGAGAAA 175
 DB 121 CCGTATTCGTTAATTGAAAGAGAAA 148

RESULT 8

ID ABV75164 standard; DNA; 148 BP.

AC ABV75164;

DT 19-FEB-2003 (first entry)

DE Crucifer tobacco mosaic virus IRES element IREScp148cr.

XX Transcription; plant; internal ribosome entry site; IRES; transgenic; ds.

OS Tobacco mosaic virus.

PN WO200283867-A2.

PD 24-OCT-2002.

PF 17-APR-2002; 2002WO-US11924.

PR 17-APR-2001; 2001US-284239P.

PA (ICON-) ICON GENETICS INC.

PI Gleba Y, Bascomb N, Bossie M, Hall G, Petty TJ;

PI WPI; 2003-067578/06.

PT Identifying and characterizing transcriptionally active regions in plants, useful for producing transgenic plants, comprises inserting nucleic acid constructs (called landing pads) with internal ribosome entry site(s) into plant genes

PT Disclosure; Page 17; 50pp; English.

XX The invention relates to identifying and characterizing transcriptionally active regions in plants. The method involves (a) inserting into the plant a genomic nucleic acid construct comprising at least one internal ribosome entry site (IRES) in operable association with a reporter gene; and (b) detecting the expression of the reporter gene as an indication of insertion of the nucleic acid construct into a transcriptionally active region. The method for identifying and characterizing transcriptionally active regions in plants, is useful for producing transgenic plants and seeds, as is the method for introducing a nucleic acid into plants. The method is also useful for observing or measuring phenotype in an organism. The present sequence represents an IRES element derived from the genome of the crucifer tobacco mosaic virus (crtmv).

XX Sequence 148 BP; 56 A; 17 C; 40 G; 35 T; 0 other;

Query Match 78.7%; Score 148; DB 25; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.5e-32; Mismatches 0; Indels 0; Gaps 0;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 GAATTCGTCGATTCGTCGACATTAAAGCGGTGACACTTTAAAGAGGAAAAAG 87
 DB 1 GAATTCGTCGATTCGTCGACATTAAAGCGGTGACACTTTAAAGAGGAAAAAG 60
 OY 88 AAGTTGAAGAAAGGCTGTAGTAAGTATTAAGTACAGACCGAGAAAGTACCCGGT 147
 DB 61 AAGTTGAAGAAAGGCTGTAGTAAGTATTAAGTACAGACCGAGAAAGTACCCGGT 120
 OY 148 CCGTATTCGTTAATTGAAAGAGAAA 175
 DB 121 CCGTATTCGTTAATTGAAAGAGAAA 148

RESULT 9

[illegible][illegible]

RESULT 11
 AAD30982/c
 ID AAD30982 standard; DNA; 6215 BP.
 XX
 AC AAD30982;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE pBSMT27 vector containing N. tabacum chloroplast gene fragment.
 XX
 KW Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP;
 KM isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
 XX transgenic plant; tobacco; ds.
 XX
 OS Nicotiana tabacum.
 XX
 PN W0200210398-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001MO-US24037.
 XX
 PR 31-JUL-2000; 2000US-221703P.
 XX
 PA (HAHN/) HAHN F M.
 XX (KUEH/) KUEHNLE A R.
 XX
 PI Hahn FM, Kuehnle AR;
 XX
 PI WPI: 2002-217122/27.
 XX
 DR Use of specific genes of mevalonate and isoprenoid biosynthetic
 PT pathways, for providing a cell with herbicide or antibiotic resistance,
 PT and for providing transformed cells having increased isoprenoid
 PT production
 PT
 XX Example 9; Page 100-103; 193pp; English.
 XX
 PS The invention relates to the use of specific genes of the mevalonate
 CC and isoprenoid biosynthetic pathways and inactive gene sites
 CC (pseudogene). Genes of the invention are used to enhance biosynthesis
 CC of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
 CC and isoprenoid pathway derived products in the plastids of transgenic
 CC plants and microalgae, for producing herbicide or antibiotic resistant
 CC transgenic plants and microalgae, for providing transformed cells with
 CC increased isoprenoid production compared to non-transformed cells, and
 CC for providing a cell with an inserted polynucleotide sequence encoding
 CC one or more products of interest. The present sequence is pBSMT27
 CC vector containing Nicotiana tabacum chloroplast gene fragment. This
 CC vector is used in the exemplification of the invention.
 XX
 SQ Sequence 6215 BP; 1667 A; 1396 C; 1268 G; 1884 T; 0 other;
 XX
 Query Match 23.1%; Score 43.4; DB 24; Length 6215;
 Best Local Similarity 57.9%; Pred. No. 0.015;
 Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 XX
 QY 1 GTGACGGTATCGATAGCTTGAATCGAATCGTCGATGCGTTGCACATTAAAGCG 60
 DB 5542 GTGACGGTATCGATAGCTTGAATCGAATCGTCGACGCCGGGGGATCCCTGAAAT 5483
 QY 61 GTTGACAACCTTTAAAGAGAAAAAGAGGTTGAAGAAAGGCTGTAGTAAGTAT 120
 DB 5482 TGGGTAGCTGTGTTAAACCGGTCGATACCTTATGAATGGTGGAGTAACAGAAAT 5423
 QY 121 AAGTACAGACCGG 133
 DB 5422 ATAGCCAGAAAGG 5410
 RESULT 12
 AAD31038/c
 ID AAD31038 standard; DNA; 7252 BP.

XX
 AC AAD31038;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Plastid transformation vector pRK07 DNA.
 XX
 KW Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP;
 KM isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
 KM transgenic plant; yeast; phosphomevalonate kinase; HMGR; AACT;
 KM mevalonate kinase; mevalonate diphosphate decarboxylase; HMG-CoA; MDP;
 KM acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
 KM MVK; PMK; HMG-CoA reductase; IPP isomerase; IPPi; ds.
 XX
 OS Chimeric - Saccharomyces cerevisiae.
 OS Chimeric - Arabidopsis thaliana.
 OS Chimeric - Rhodobacter capsulatus.
 XX
 PN W0200210398-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001MO-US24037.
 XX
 PR 31-JUL-2000; 2000US-221703P.
 XX
 PA (HAHN/) HAHN F M.
 XX (KUEH/) KUEHNLE A R.
 XX
 PI Hahn FM, Kuehnle AR;
 XX
 PI WPI: 2002-217122/27.
 XX
 DR Use of specific genes of mevalonate and isoprenoid biosynthetic
 PT pathways, for providing a cell with herbicide or antibiotic resistance,
 PT and for providing transformed cells having increased isoprenoid
 PT production
 PT
 XX Claim 77; Page 169-173; 193pp; English.
 XX
 PS The invention relates to the use of specific genes of the mevalonate
 CC and isoprenoid biosynthetic pathways and inactive gene sites
 CC (pseudogene). Genes of the invention are used to enhance biosynthesis
 CC of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
 CC and isoprenoid pathway derived products in the plastids of transgenic
 CC plants and microalgae, for producing herbicide or antibiotic resistant
 CC transgenic plants and microalgae, for providing transformed cells with
 CC increased isoprenoid production compared to non-transformed cells, and
 CC for providing a cell with an inserted polynucleotide sequence encoding
 CC one or more products of interest. The present sequence is plastid
 CC transformation vector pRK07 containing operon C DNA which encodes the
 CC entire mevalonate pathway. This operon contains S. cerevisiae orfs
 CC encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK),
 CC mevalonate diphosphate decarboxylase (MDP), acetoacetyl thiolase (AACT),
 CC A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A
 CC (HMG-CoA) synthase (HMG5), HMG-CoA reductase (HMGR) and R. capsulatus
 CC orf encoding IPP isomerase (IPPI).
 XX
 SQ Sequence 7252 BP; 1820 A; 1719 C; 1653 G; 2060 T; 0 other;
 XX
 Query Match 23.1%; Score 43.4; DB 24; Length 7252;
 Best Local Similarity 57.9%; Pred. No. 0.015;
 Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 XX
 QY 1 GTGACGGTATCGATAGCTTGAATCGAATCGTCGATGCGTTGCACATTAAAGCG 60
 DB 6579 GTGACGGTATCGATAGCTTGAATCGAATCGTCGACGCCGGGGGATCCCTGAAAT 6520
 QY 61 GTTGACAACCTTTAAAGAGAAAAAGAGGTTGAAGAAAGGCTGTAGTAAGTAT 120
 DB 6519 TGGGTAGCTGTGTTAAACCGGTCGATACCTTATGAATGGTGGAGTAACAGAAAT 6460
 QY 121 AAGTACAGACCGG 133

Patent No. 5670367

GENERAL INFORMATION:

```

      APPLICANT: ENTIAN, Karl-Dieter
      TITLE OF INVENTION: Process for Screening Antimycotically Active Substances
      FILE REFERENCE: 38005-0094
      CURRENT APPLICATION NUMBER: US/09/402,266B
      PRIOR FILING DATE: 1999-10-08
      PRIOR APPLICATION NUMBER: PCT/EP98/01904
      PRIOR FILING DATE: 1998-10-08
      PRIOR APPLICATION NUMBER: DE 19713572.2
      PRIOR FILING DATE: 1997-04-02
      NUMBER OF SEQ ID NOS: 38
      SOFTWARE: PatentIn version 3.0
      SEQ ID NO 20
      LENGTH: 4102
      TYPE: DNA
      ORGANISM: Unknown
      FEATURE:
      NAME/KEY: misc.feature
      LOCATION: ().()
      OTHER INFORMATION: Synthetic sequence
      *US-09-402-266B-20

Query Match
Best Local Similarity 20.6%; Score 38.8; DB 4; Length 4102;
Matches 76; Conservative 0; Mismatches 42; Indels 2; Gaps 1;

QY 1 GTCGACGTCATCGATTAACCTGGATATCGAATTCGTGATCGGTGCAGCATTTAAACG 60
DB 1876 GTCCGACGTCATCGAATACCTGGATATCGAATTCCTGCAGCGGCCCAACATGAGAAATG 181
QY 61 GTGCACACTTTAAAGAAAGAAAAAGAGGTGAGAAAAAGGGTGTAAGTAAGTAT 120
DB 1816 GGTATTAATCTG-ATATATTAATTAATGAAGCTCTAATTTGTGAGTTAGTATACATGCAT 1759

RESULT 4
US-09-144-918-3/C
Sequence 3, Application US/09144918
Patient No. 6287807
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: MAF
FILE REFERENCE: GM10098
CURRENT APPLICATION NUMBER: US/09/144,918
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/060,682
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1094
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (497)...(1094)
US-09-144-918-3

Query Match
Best Local Similarity 20.1%; Score 37.8; DB 3; Length 1094;
Matches 45; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GTCGACGTCATCGATTAAGCTTGATATCGAATTCGTGATTCGGTTGCAGCATTTAA 57
DB 1062 GTCCGACGTCATCGAATACCTGGATATCGAATTCCTGCAGCGCCGTCGCAATTTTCATA 1006

RESULT 5
US-08-928-799A-4
Sequence 4, Application US/08928799A
Patient No. 6069302
GENERAL INFORMATION:
APPLICANT: Osborn, Thomas C
APPLICANT: Buttrille, David V

```

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Version #1.30
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/928,799A
8 FILING DATE:
9 CLASSIFICATION: 800
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Berson, Bennett J
12 REGISTRATION NUMBER: 37094
13 REFERENCE/DOCKET NUMBER: 960296,94240
14 TELEPHONE: 608-251-5000
15 TELEFAX: 608-251-9166
16 INFORMATION FOR SEQ ID NO: 4:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 516 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: double
21 TOPOLOGY: linear
22 MOLECULE TYPE: DNA (genomic)
23 ORIGINAL SOURCE:
24 ORGANISM: Brassica napus
25 IMMEDIATE SOURCE:
26 CLONE: W67B3.T7
27 FEATURE:
28 NAME/KEY: primer_bind
29 LOCATION: 358..377
30 US-08-928-799A-4
31
32 Query Match 20.0%; Score 37.6; DB 3; Length 516;
33 Best Local Similarity 72.1%; Pred. No. 0.018;
34 Matches 49; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
35
36 Oy 1 GTTCACGGTATCATGATTCGATTCGAAATTCGTCGATTCGGTTCGACGATTTAAAGC 60
37 Db 22 GTTCACGGTATCATGATTCGATTCGAAATTCGTCGATTCGGTTCGACGATTTAAAGC 81
38 Oy 61 GTTGACAA 68
39 Db 82 GACACAA 89
40
41 RESULT 6
42 US-08-553-367A-5
43 Sequence 5, Application US/08553367A
44 Patent No. 5939539
45 GENERAL INFORMATION:
46 APPLICANT: Theodor LANGE et al.
47 TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
48 NUMBER OF SEQUENCES: 19
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
51 STREET: 2033 K Street, N.W., Suite 800
52 CITY: Washington
53 STATE: D.C.
54 COUNTRY: U.S.A.
55 ZIP: 20006
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
58 COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 593953September 27, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40, 949
REFERENCE/DOCKET NUMBER: 49/EPD.5M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PAT2353
US-08-553-367A-5

Query Match          20.0%; Score 37.6; DB 2; Length 1490;
Best Local Similarity 65.5%; Pred. No. 0.025;
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0

QY      7  GGTATCGATAAGCTTGATATCGAAATTCGTCGATTGCGTTGAGCAGCATTTAAAGCGGTGAC 66
          |||||
          1  GGTATCATATAAGCTTGATATCGAAATTCGAGGATCCGAGCATGTGACAAAACCCCAAA 60
QY      67  AACTTAAAGAGAGAAAAGAG 90
          |||||
          DB 61  CTCCTAAGAAAAAAGAGAG 84

RESULT 7
US-09-295-306-5
Sequence 5, Application US/09295306
Patent No. 6198021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:

```

NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/DIV-FDA-5M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PAT2353
US-09-295-306-5

Query Match 20.0%; Score 37.6; DB 3; Length 1490;
Best Local Similarity 65.5%; Pred. No. 0.025;
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 7 GGATGATTAAGCTTATATCGAATTCGTCGATTCGTCGACATTAAAGCGGTTGAC 66
|||||
DB 1 GGATGATTAAGCTTATATCGAATTCGTCGATTCGTCGACATTAAAGCGGTTGAC 60
|||||

QY 67 AACTTAAAGAAGAAAAAGAG 90
|||
DB 61 CTCTCAAGAAAAAGAAAAAG 84
|||

RESULT 8
US-09-734-719-5
Sequence 5, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6455675,ember 27, 1995
APPLICATION NUMBER: PCT/EP94/01664
FILING DATE: May 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PAT2353
US-09-734-719-5

Query Match 20.0%; Score 37.6; DB 4; Length 1490;
Best Local Similarity 65.5%; Pred. No. 0.025;
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 7 GGATGATTAAGCTTATATCGAATTCGTCGATTCGTCGACATTAAAGCGGTTGAC 66
|||||
DB 1 GGATGATTAAGCTTATATCGAATTCGTCGATTCGTCGACATTAAAGCGGTTGAC 60
|||||

QY 67 AACTTAAAGAAGAAAAAGAG 90
|||
DB 61 CTCTCAAGAAAAAGAAAAAG 84
|||

RESULT 9
US-08-352-902D-146
Sequence 146, Application US/08352902D
Patent No. 6191268
GENERAL INFORMATION:
APPLICANT: Liskay, Robert M.
Brunner, C. Eric
Baker, Sean M.
Boilag, Roni J.
Kolodner, Richard D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & Heuser
STREET: 520 S.W. Yamhill Street, Suite 200
CITY: Portland
STATE: Oregon
COUNTRY: U.S.A.
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,902D
FILING DATE: 09-Dec-1994
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: OHSU 306B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-6655
TELEFAX: (503) 295-6679
TELEX: 360619
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 821 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
POSITION IN GENOME:
MAP POSITION: Human Chromosome 7q
SEQUENCE DESCRIPTION: SEQ ID NO: 146
US-08-352-902D-146

Query Match 19.4%; Score 36.4; DB 3; Length 821;
Best Local Similarity 97.4%; Pred. No. 0.048;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATAGCTTGATATCGAATTCGTCGATTCGGTGGACGATTAA 38
DB 12 GTGACGGTATCGATAGCTTGATATCGAATTCGTCGATTCGGTGGACGATTAA 49

RESULT 10

US-08-928-799A-2
Sequence 2, Application US/08928799A
Patent No. 6069302

GENERAL INFORMATION:

APPLICANT: Osborn, Thomas C
TITLE OF INVENTION: Hybrid Spring Oilseed Brassica napus
TITLE OF INVENTION: With Winter Germplasm Introgression
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plinckney St
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,799A
FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Beeson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.94240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 474 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE: Brassica napus

IMMEDIATE SOURCE: Brassica napus

CLONE: WGB10.T7

FEATURE:

NAME/KEY: primer blind

LOCATION: 146..165

US-08-928-799A-2

Query Match 19.3%; Score 36.2; DB 3; Length 474;
Best Local Similarity 77.2%; Pred. No. 0.047;
Matches 44; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATAGCTTGATATCGAATTCGTCGATTCGGTGGACGATTAA 57
DB 23 GTGACGGTATCGATAGCTTGATATCGAATTCGTCGATTCGGTGGACGATTAA 79

RESULT 11
US-08-838-219B-8/c
Sequence 8, Application US/08838219B
Patent No. 5877012

GENERAL INFORMATION:

APPLICANT: Warren, Gregory M
APPLICANT: Koziet, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J

TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
TITLE OF INVENTION: Control of Plant Pests
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,219B
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/463,483

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594

FILING DATE: 09-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/218,018

FILING DATE: 23-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40,403

REFERENCE/DOCKET NUMBER: CGC 1925

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8689

TELEFAX: 919-541-8682

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1638 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 2..1191

OTHER INFORMATION: /Product- "Translation of cDNA

OTHER INFORMATION: encoding VIP3a(a) receptor"

US-08-838-219B-8

Query Match 18.9%; Score 35.6; DB 2; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATAGCTTGATATCGAATTCGTCGATTCGGTGGACGATTAA 60

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1191
OTHER INFORMATION: /product- "translation of CDNA
US-09-233-752A-8 encoding VIP3A(a) receptor"

Query Match 18.9%; Score 35.6; DB 3; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60
DB 1633 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60
QY 61 GTTGACAACTTTAA 74
DB 1573 CTTATATAATTTTAA 1560

RESULT 14
US-09-402-036-8/c
Sequence 8, Application US/09402036
Patent No. 6291156
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Yu, Cao-Guo
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalini
APPLICANT: Koziel, Michael
APPLICANT: Nye, Gordon
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284C
CURRENT APPLICATION NUMBER: US/09/402,036
CURRENT FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,265
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/463,483
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/314,594
PRIOR FILING DATE: 1994-09-09
PRIOR APPLICATION NUMBER: 08/218,018
PRIOR FILING DATE: 1994-03-24
PRIOR APPLICATION NUMBER: 08/037,057
PRIOR FILING DATE: 1993-03-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1638
TYPE: DNA
ORGANISM: Agrotis ipsilon
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1189)
OTHER INFORMATION: translation of CDNA encoding VIP3A(a) receptor
US-09-402-036-8 OTHER INFORMATION: from Black cutworm

Query Match 18.9%; Score 35.6; DB 3; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60
DB 1633 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60

QY 61 GTTGACAACTTTAA 74
DB 1573 CTTATATAATTTTAA 1560

RESULT 15
US-09-904-226-8/c
Sequence 8, Application US/09904226
Patent No. 6429360
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalini
APPLICANT: Koziel, Michael
APPLICANT: Nye, Gordon
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284D
CURRENT APPLICATION NUMBER: US/09/904,226
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,265
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/463,483
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/314,594
PRIOR FILING DATE: 1994-09-09
PRIOR APPLICATION NUMBER: 08/218,018
PRIOR FILING DATE: 1994-03-24
PRIOR APPLICATION NUMBER: 08/037,057
PRIOR FILING DATE: 1993-03-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1638
TYPE: DNA
ORGANISM: Agrotis ipsilon
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1189)
OTHER INFORMATION: translation of CDNA encoding VIP3A(a) receptor
US-09-904-226-8 OTHER INFORMATION: from Black cutworm

Query Match 18.9%; Score 35.6; DB 4; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60
DB 1633 GTCGACGGTATCGATACCTTGATATCGAATTCGTGATTCGTTGCACGATTAAAGCG 60
QY 61 GTTGACAACTTTAA 74
DB 1573 CTTATATAATTTTAA 1560

Search completed: September 26, 2003, 10:16:57
Job time : 67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 08:40:24 ; Search time 256 Seconds

(without alignments)
1828.220 Million cell updates/sec

Title: US-09-758-962-1

Perfect score: 188

Sequence: 1 gtcgacggtatcgataagct.....gaagaagaagcaccatg 188

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCF_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCFUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	188	11	US-09-758-962-1
2	181	96.3	181	11	US-09-758-962-5
3	165	87.8	181	11	US-09-758-962-7
4	151.4	80.5	180	11	US-09-758-962-6
5	150	79.8	187	11	US-09-758-962-3
6	149	79.3	251	11	US-09-758-962-2
7	148	78.7	148	14	US-10-165-420-2
8	148	78.7	796	12	US-10-211-079-19
9	90	47.9	796	12	US-10-386-708-18
10	90	47.9	799	12	US-10-211-079-23
11	90	47.9	799	12	US-10-356-708-22
12	90	47.9	808	12	US-10-211-079-22
13	88.8	47.2	1543	12	US-10-356-708-21
14	88.8	47.2	1543	12	US-10-236-508-17
15	88.8	47.2	1543	14	US-10-133-934-9
16	88.8	47.2	1543	14	US-10-105-697-9

17	88.8	47.2	1543	14	US-10-120-630-9	Sequence 9, Appl
18	88.8	47.2	1543	14	US-10-137-765-23	Sequence 23, Appl
19	88.8	47.2	1543	14	US-10-146-337-23	Sequence 23, Appl
20	88.8	47.2	1543	14	US-10-146-337-23	Sequence 31, Appl
21	81	43.1	1536	14	US-10-072-438-31	Sequence 31, Appl
22	43.4	23.1	6215	11	US-09-918-740-17	Sequence 17, Appl
23	43.4	23.1	7252	11	US-09-918-740-17	Sequence 73, Appl
24	43.4	23.1	7252	11	US-09-918-740-75	Sequence 75, Appl
25	43.4	23.1	13917	11	US-09-918-740-72	Sequence 72, Appl
26	40.2	21.4	5616	10	US-09-924-035A-40	Sequence 430, App
27	39.8	21.2	418	10	US-09-924-035A-634	Sequence 634, App
28	39.2	20.9	327	10	US-09-924-035A-52	Sequence 52, Appl
29	39	20.7	456	12	US-09-924-035A-15014	Sequence 15014, A
30	38.4	20.4	382	10	US-09-924-035A-720	Sequence 720, App
31	38.4	20.4	781	14	US-10-198-846-4407	Sequence 4407, Ap
32	38	20.2	434	10	US-09-924-035A-656	Sequence 656, App
33	38	20.2	455	10	US-09-924-035A-730	Sequence 730, App
34	38	20.2	616	11	US-09-776-724A-62	Sequence 62, Appl
35	37.8	20.1	587	14	US-09-932-418-35	Sequence 35, Appl
36	37.8	20.1	1094	10	US-09-932-418-3	Sequence 3, Appl
37	37.8	20.1	122	11	US-09-814-353-13335	Sequence 13335, A
38	37.4	19.9	319	12	US-09-814-353-13302	Sequence 13302, A
39	37.4	19.9	458	12	US-10-001-189-53	Sequence 53, Appl
40	37	19.7	4941	13	US-08-935-377-7	Sequence 7, Appl
41	36.6	19.5	148	9	US-09-822-250-7	Sequence 3, Appl
42	36.6	19.5	148	10	US-09-987-456-3	Sequence 5, Appl
43	36.6	19.5	148	11	US-09-818-991-5	Sequence 152, App
44	36.6	19.5	148	11	US-10-052-942-152	
45	36.6	19.5	148	14	US-10-052-942-152	

ALIGNMENTS

US-09-758-962-1	RESULT 1
Sequence 1, Application US/09758962	
Publication No. US20030049228A1	
GENERAL INFORMATION:	
APPLICANT: SANTA CRUZ, SIMON	
APPLICANT: TOTI, RACHAEL L.	
APPLICANT: CHAPMAN, SEAN	
APPLICANT: CARR, FIONA	
APPLICANT: ROGUE, GREGORY	
TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF FOREIGN GENES FROM PLANT VIRUS VECTORS	
FILE REFERENCE: 008010192NPUS00	
CURRENT APPLICATION NUMBER: US/09/758,962	
CURRENT FILING DATE: 2001-01-09	
NUMBER OF SEQ ID NOS: 8	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 1	
LENGTH: 188	
TYPE: DNA	
ORGANISM: Potato virus	
US-09-758-962-1	
Query Match	100.0%; Score 188; DB 11; Length 188;
Best Local Similarity	100.0%; Pred. No. 1.6e-43;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GTCGACGGTATCGATAGCTGATATCGAATCGTCGATCGCAGCATTTAAAGC 60
DB	1 GTCGACGGTATCGATAGCTGATATCGAATCGTCGATCGCAGCATTTAAAGC 60
QY	61 GTTCAACACTTTAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 120
DB	61 GTTCAACACTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 120
QY	121 AAGTCAACACCGGAGAGATAGCCGCTGCTGTTGTTTAAATTGAAGAGAGAGCT 180
DB	121 AAGTCAACACCGGAGAGATAGCCGCTGCTGTTGTTTAAATTGAAGAGAGAGCT 180

OY	181	CACCATGG	188
Db	181	CACCATGG	188

RESULT 2
ME-09-7E

```

Sequence 5, Application US/09758962
Publication No. US20030049228A1
GENERAL INFORMATION:
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTTH, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
APPLICANT: CARR, FIONA
APPLICANT: POGUE, GREGORY
TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
FILE REFERENCE: 008010192NPUS00
CURRENT APPLICATION NUMBER: US/09/758,962
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO. 5
LENGTH: 181
TYPE: DNA
ORGANISM: Potato virus
US-09-758-962-5

```

Query Match	96.3%	Score 181;	DB 11;	Length 181;
Best Local Similarity	100.0%	Pred. No. 1,4e-41;		
Matches 181; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	GTGCACGGGATGATGAAATGCTTGATTCGAATTCGCGATTCGGTGGAGCATTTAAAGCG	50
Db	1	GTGCACGGGATGATGAAATGCTTGATTCGAATTCGCGATTCGGTGGAGCATTTAAAGCG	60
QY	61	GTTCACAACTTTAAAGAAGGAAAAAGAAGTTGAGAAAAAGCGTGTAGTAAGTAAGTAT	120
Db	61	GTTCACAACTTTAAAGAAGGAAAAAGAAGTTGAGAAAAAGCGTGTAGTAAGTAAGTAT	120
QY	121	AAGTACACAGCGGAGAAATACGCCGGTCTCTATTCGTTAATTTGAAAGAAAGAGCT	180
Db	121	AAGTACACAGCGGAGAAATACGCCGGTCTCTATTCGTTAATTTGAAAGAAAGAGCT	180
QY	181	C 181	
Db	181	C 181	

RESULT 3
PC-09-751

```

Sequence: 7, Application: US/09758962
Publication No.: US2003003049228A1
GENERAL INFORMATION:
Applicant: SANTA CRUZ, SIMON
Applicant: TOTI, RACHAEL L.
Applicant: CHAPMAN, SEAN
Applicant: CARR, ETIQA
Applicant: POGUE, GREGORY
Title of Invention: A NOVEL STRATEGY FOR THE EXPRESSION OF
Title of Invention: FOREIGN GENES FROM PLANT VIRUS VECTORS
File Reference: 008010192NPUS00
Current Application Number: US/09/7758,962
Current Filing Date: 2001-01-09
Number of SEQ ID NOS: 8
Software: FastSeq for Windows Version 4.0
SEQ ID NO 7
Length: 181
Type: DNA
Organism: Potato virus
US-09-758-962-7

```

Query Match 87.88; Score 165; DB 11; Length 181;

Best Local Similarity 94.5%; Pred. No. 4.7e-37;
Matches 171; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	GTCGACGGATCGATTAAGCTTCAATTCGCAATTCGGTATGGCAGCAATTTAAAGCG	60
Db	1	GTCGACGGATTCGATTAAGCTTCAATTCGCAATTCGGTATGGCAGCAATTTAAAGCG	60
QY	61	GTTGACAACTTTAAAAGAGAAAAAGAGGTTGAGAAAAAGGTAGTAAGTAAGTAT	120
Db	61	GTTGACAACTTTAAAAGAGAAAAAGAGGTTGAGAAAAAGGAGTAGTAAGTAAGTAT	120
QY	121	AAGTACAGACCGGAGAGTAGCCCGCTCTGATTCGTTAATTGGAAGAAGAAAGACT	180
Db	121	AAGTACAGACCGGAGAGTAGCCCGCTCTGATTCGTTAATTGGAAGAAGAGAGCT	180
QY	181	C 181	
Db	181	C 181	

RESULT 4

```

1 Sequence 6, Application US/09758962
2 Publication No. US20030049228A1
3 GENERAL INFORMATION:
4 APPLICANT: SANTA CRUZ,
5 APPLICANT: TOTTH, RACHAEL L.
6 APPLICANT: CHAPMAN, SEAN
7 APPLICANT: CARR, FIONA
8 APPLICANT: POGUE, GREGORY
9 TITLE OF INVENTION: A NOVEL STRATEGY FOR
10 TITLE OF INVENTION: FOREIGN GENES FROM P
11 FILE REFERENCE: 008010192NPUS00
12 CURRENT APPLICATION NUMBER: US/09/758,962
13 CURRENT FILING DATE: 2001-01-09
14 NUMBER OF SEQ ID NOS: 8
15 SOFTWARE: FASTSEQ for Windows Version 4.0.
16 SEQ ID NO 6
17 LENGTH: 180
18 TYPE: DNA
19 ORGANISM: Potato virus
20 US-09-758-962-6

```

Query Match	80.5%;	Score 151.4;	DB 11;	Length 180;
Best Local Similarity	93.4%;	Pred. No. 3.2e-33;		
Matches 169; Conservative	0;	Mismatches 11;	Indels 1;	Gaps 1;

QY	1	GTGCGAGGATGCGATTAAGCTTGATATACGAATTCGTCGATTCCGTTGCACATTTAAGG	60
Db	1	GTGCGAGGATGCGATTAAGCTTGATATACGAACTCGCCGATTCCGGTGTGCA-TTAAAGCG	59
QY	61	GTTCACAACCTTTAAAAGAGAAAAAGAGTTGAAGAAAAAGGTGTAGTAGTAGTAT	12
Db	60	GCTGACAAACCTTTAAAAGAGAAAAAGAGGTTGAAGAAAAAGGTGTAGTAGTAGTAT	11
QY	121	AAGTACAGACCGGAGAGTAGCCCGCTCGATTGCTTTAATTGAAGAAAGAGCT	18
Db	120	AAGTACAGACCGGCGAAGTGCCTCGATTGCTTTAATTGAAGAAAGAGAGCT	17
QY	181	C 181	
Db	180	C 180	

RESULT 5

Sequence 3, Application US/09758962
Publication No. US20030049228A1
GENERAL INFORMATION:
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTI, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
APPLICANT: CARR, ETIENA

```

; APPLICANT: POGUE, GREGORY
; TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
; FILE REFERENCE: FOREIGN GENES FROM PLANT VIRUS VECTORS
; CURRENT APPLICATION NUMBER: 008010192NPUS00
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 187
; TYPE: DNA
; ORGANISM: Potato virus
; US-09-758-962-3

Query Match      79.8%; Score 150; DB 11; Length 187;
Best Local Similarity 96.8%; Pred. No. 8e-33;
Matches 153; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 29 AATCGTGATTCGGTTCGACATTTAAAGCGGTGACACTTTAAAGAGGAAAAAGA 88
    |||||||
Db 180 AATCGTGATTCGGTTCGACATTTAAAGCGGTGACACTTTAAAGAGGAAAAAGA 121

QY 89 AGCTGAGAAAAAGGCTAGTAAAGTATAGTACAGCGGAGAGTACCGCGGTC 148
    |||||||
Db 120 AGCTGAGAAAAAGGCTAGTAAAGTATAGTACAGCGGAGAGTACCGCGGTC 61

QY 149 CTGATTCGTTTAATTGAAAGAGAAAGCTCACCAT 186
    |||||||
Db 60 CTGATTCGTTTAATTGAAAGAGAAAGTTCGATAT 23

RESULT 6
US-09-758-962-2
; Sequence 2, Application US/09758962
; Publication No. US20030049228A1
; GENERAL INFORMATION:
; APPLICANT: SANTA CRUZ, SIMON
; APPLICANT: TOTH, RACHAEL L.
; APPLICANT: CHAPMAN, SEAN
; APPLICANT: CARR, FIONA
; APPLICANT: POGUE, GREGORY
; TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
; FILE REFERENCE: FOREIGN GENES FROM PLANT VIRUS VECTORS
; CURRENT APPLICATION NUMBER: US/09/758,962
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 251
; TYPE: DNA
; ORGANISM: Potato virus
; US-09-758-962-2

Query Match      79.3%; Score 149; DB 11; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.7e-32;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CGAATTCGTCGATTCGGTTCGACATTTAAAGCGGTGACAACTTTAAAGAGGAAAA 86
    |||||||
Db 97 CGAATTCGTCGATTCGGTTCGACATTTAAAGCGGTGACAACTTTAAAGAGGAAAA 156

QY 87 GAGGTTGAGAAAAAGGCTAGTAAAGTATAGTACAGACCGGAGAGTACCGCGG 146
    |||||||
Db 157 GAGGTTGAGAAAAAGGCTAGTAAAGTATAGTACAGACCGGAGAGTACCGCGG 216

QY 147 TCCTGATTCGTTTAATTGAAAGAGAA 175
    |||||||
Db 217 TCCTGATTCGTTTAATTGAAAGAGAA 245

RESULT 7
US-10-165-420-2
```

```

; Sequence 2, Application US/10165420
; Publication No. US20030084482A1
; GENERAL INFORMATION:
; APPLICANT: HALL, GERALD
; APPLICANT: BASCOMB, NEWELL
; APPLICANT: BOSSIE, MARK
; TITLE OF INVENTION: PRODUCTION OF PROTEINS IN PLANTS
; FILE REFERENCE: 57717 (71758)
; CURRENT APPLICATION NUMBER: US/10/165,420
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/297,103
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Tobacco mosaic virus
; OTHER INFORMATION: CTMV
; US-10-165-420-2

Query Match      78.7%; Score 148; DB 14; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.7e-32;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GAATTCGTCGATTCGGTTCGACATTTAAAGCGGTGACACTTTAAAGAGGAAAAAG 87
    |||||||
Db 1 GAATTCGTCGATTCGGTTCGACATTTAAAGCGGTGACACTTTAAAGAGGAAAAAG 60

QY 88 AAGTTGAGAAAAAGGCTAGTAAAGTATAGTACAGACCGGAGAGTACCGCGGT 147
    |||||||
Db 61 AAGTTGAGAAAAAGGCTAGTAAAGTATAGTACAGACCGGAGAGTACCGCGGT 120

QY 148 CCGATTCGTTTAATTGAAAGAGAA 175
    |||||||
Db 121 CCGATTCGTTTAATTGAAAGAGAA 148

RESULT 8
US-10-211-079-19
; Sequence 19, Application US/10211079
; Publication No. US20030148315A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Hal S.
; APPLICANT: Vaeyhongs, Andrew A.
; APPLICANT: Vojdani, Fakhrieh S.
; APPLICANT: Smith, Mark L.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding CEL I
; FILE REFERENCE: P-IG 5381
; CURRENT APPLICATION NUMBER: US/10/211,079
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 10/098,155
; PRIOR FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 796
; TYPE: DNA
; ORGANISM: tobamovirus
; US-10-211-079-19

Query Match      47.9%; Score 90; DB 12; Length 796;
Best Local Similarity 73.0%; Pred. No. 1.1e-15;
Matches 130; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 GTCGACGTAATCGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
    |||||||
Db 544 GTCGACGTTTCGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 603

QY 61 GTGACAACTTTAAAGAGGAAAAAGAGGTTGAGAGGAGGAGGAGGAGGAGGAGGAGG 117
    |||||||
```



```
FILE REFERENCE: P-LG 5381
CURRENT APPLICATION NUMBER: US/10/211,079
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 10/098,155
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 808
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-211-079-22

Query Match
Best Local Similarity 73.0%; Score 90; DB 12; Length 808;
Matches 130; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

1 GTCGACGGTATCGATAGCTTGATATCGAATTCGTGATTCGGTTGCAGCATTTAAAGCG 60
|||||
556 GTCGAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTGCAGCATTTCAAGCG 615
|||||

61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTGTA---GTAAGTAAG 117
|||||
616 GTTGACACTTTCAAGAGAGAAAAAGAGATTCGAGAGAAAGATGAATTAATTAAG 675
|||||

118 TATAAGTACAGACCGAGAGATGACCGGTCTGATTCGTTAATTGGAAGAGAAA 175
|||||
676 TTGAGATTAAGACCGAGAGATGACCGGTCTGATTCGTTAATTGAAGAGAAA 733
|||||

RESULT 13
US-10-356-708-21
; Sequence 21, Application US/10356708
; Publication No. US20030157682A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: MISMATCH ENDONUCLEASES AND METHODS OF USE THEREOF
FILE REFERENCE: P-LG 10100
CURRENT APPLICATION NUMBER: US/10/356,708
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 10/098,155
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 10/211,079
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 808
TYPE: DNA
ORGANISM: Artificial Sequence derived from tomato mosaic virus and TMV-Cg
FEATURE:
OTHER INFORMATION: This sequence was derived by shuffling in accordance with the met
US-10-356-708-21

Query Match
Best Local Similarity 47.9%; Score 90; DB 12; Length 808;
Matches 130; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

1 GTCGACGGTATCGATAGCTTGATATCGAATTCGTGATTCGGTTGCAGCATTTAAAGCG 60
|||||
556 GTCGAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTGCAGCATTTCAAGCG 615
|||||

61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTGTA---GTAAGTAAG 117
|||||
616 GTTGACACTTTCAAGAGAGAAAAAGAGATTCGAGAGAAAGATGAATTAATTAAG 675
|||||

118 TATAAGTACAGACCGAGAGATGACCGGTCTGATTCGTTAATTGGAAGAGAAA 175
|||||
676 TTGAGATTAAGACCGAGAGATGACCGGTCTGATTCGTTAATTGAAGAGAAA 733
|||||
```

```
Db
676 TTGAGATTAAGACCGAGAGATGACCGGTCTGATTCGTTAATTGAAGAGAAA 733

RESULT 14
US-10-236-508-17
; Sequence 17, Application US/10236508
; Publication No. US20030167512A1
GENERAL INFORMATION:
APPLICANT: Monto H. Kumagai
APPLICANT: Guy R. della-Cioppa
APPLICANT: Robert L. Erwin
APPLICANT: David R. McGee
TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY A
TITLE OF INVENTION: TRANSFECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A
TITLE OF INVENTION: DIFFERENT HOST PLANT IN A POSITIVE ORIENTATION
FILE REFERENCE: 0080101370505
CURRENT APPLICATION NUMBER: US/10/236,508
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 1543
TYPE: DNA
ORGANISM: Ribgrass mosaic virus (RMV)
US-10-236-508-17

Query Match
Best Local Similarity 47.2%; Score 88.8; DB 12; Length 1543;
Matches 133; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

1 GTCGACGGTATCGATAGCTTGATATCGAATTCGTGATTCGGTTGCAGCATTTAAAGCG 60
|||||
657 GTCGAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTGCAGCATTTCAAGCG 716
|||||

61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTGTA---GTAAGTAAG 117
|||||
717 ATTGACAGTTCCGAAGAGAGAAAAAGAGATTCGAGAGAGGATGAATTAATTAAG 776
|||||

118 TATAAGTACAGACCGAGAGATGACCGGTCTGATTCGTTAATTGGAAGAGAAA 177
|||||
777 TATAAGTATGACCGAGAGATGACCGGTCTGATTCGTTAATTAATTAAGAGAAAAT 836
|||||

178 GCTCACCA 185
| | |
837 GGTTCACA 844

RESULT 15
US-10-133-934-9
; Sequence 9, Application US/10133934
; Publication No. US20030024008A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Monto H.
APPLICANT: della-Cioppa, Guy R.
APPLICANT: Erwin, Robert L.
APPLICANT: McGee, David R.
TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A
TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF A
TITLE OF INVENTION: TRANSFECTING A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
FILE REFERENCE: 0080101370504
CURRENT APPLICATION NUMBER: US/10/133,934
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US/09/359,301A
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1543
TYPE: DNA
ORGANISM: Ribgrass mosaic virus
US-10-133-934-9
```


LOCUS	AW740521	254 bp	mRNA	linear	EST 27-APR-2000
DEFINITION	BRL10478 Biomphalaria glabrata (BS-90)-unexposed lambda Zap library				
VERSION	AW740521.1				
KEYWORDS	AM740521.1 GI:7651614				
SOURCE	EST				
ORGANISM	Biomphalaria glabrata (bloodfluke planorb)				
REFERENCE	Biomphalaria glabrata Eukaryote; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora				
AUTHORS	1 (bases 1 to 254) Raghavan,N., Miller,A.N., Gardner,M., Fitzgerald,P.C., Kerlavage				
TITLE	A.R., Johnston,D.A., Lewis,F.A. and Knight,M.				
JOURNAL	Comparative gene analysis of Biomphalaria glabrata hemocytes pre-				
MEDLINE	and post-exposure to miracidia of Schistosoma mansoni				
PUBMED	Mol. Biochem. Parasitol. 126 (2), 181-191 (2003)				
COMMENT	22503446 12615317. Contact: Raghavan N Biomedical Research Institute 1211 Parklawn Dr., Rockville, MD 20852, USA Tel: 301-881-3300 ext.128 Fax: 301-770-4756 Email: nkrhelix.nih.gov, smallsrule@aol.com. Location/Qualifiers 1. 254 /organism="Biomphalaria glabrata" /mol_type="mRNA" /strain="BS-90" /db_xref="taxon:6526" /clone="RBGIG26TR" /sex="hermaphrodite" /cell_type="hemocyte" /lab_host="laboratory host" /clone_lib="Biomphalaria glabrata (BS-90)-unexposed lambda zap library" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Total RNA was isolated from the hemocytes of unexposed Biomphalaria glabrata (BS-90) snails and first strand cDNA synthesized using an oligo-dT primer-linker (xhoI). Second strand synthesis was followed by the ligation of EcoRI adaptors. Following digestion with XhoI, the completed, directional cDNA was cloned into Uni-Zap XR plasmid vector by Stratgene."				
BASE COUNT	62 a 47 c 59 g 86 t				
ORIGIN					
Query Match	23.48;	Score 44;	DB 9;	Length 254;	
Best Local Similarity	61.1%;	Pred. No. 13;			
Matches	88;	Conservative	0;	Mismatches	55; Indels 1; Gaps 1;
Y	1	GTCGACGGATGTGAATAAGCTGTATATCGCAATTCCGTCGATT-CGGTTGCACATTAAACC	59		
b	254	GTTCGACGGATGTGAATAAGCTGTATATCGCAATTCCGTCGACGACTCGGCCGAATTCGGCAC	195		
y	60	GCGTGACAACCTTAAGAAGAAAAAAGAGGTTGAGAAAAGGGGTGCTAGTAGTAAGTA	119		
b	194	GAGTTACACATCCACATTAACAGCGCGTNTGAAAGTCCAAGACGATTAGTTACAGAGTAATCA	135		
y	120	TAACTACAGACCCGAGAAAGTACGC	143		
b	134	CNAAGTAAGCTCCGCAACACACAGCCG	111		
RESULT 5	UT91304/c				
OCUS	BU791304	668 bp	mRNA	linear	EST 12-FEB-2003
DEFINITION	STFRAG07 SJF Schistosoma japonicum DNA, mRNA sequence.				
ACCESSION	BU791304				
VERSION	BU791304.1	GI:28348311			
KEYWORDS	EST				
SOURCE	Schistosoma japonicum				
ORGANISM	Schistosoma japonicum				

	REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
	AUTHORS	Strigiledda, Schistosomatidae; Schistosomatidae; Schistosoma.
	TITLE	1 (bases 1 to 668)
JOURNAL COMMENT		Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z., Huang,T., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han,Z.
FEATURES		Expressed sequence tags from female adults of Schistosoma japonicum Unpublished
SOURCE	Contact:	Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhanglejiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex. 45) Fax: 86-21-50801922 Email: hanzge@nc.sh.cn
	Location/Qualifiers	1..668
BASE COUNT	/organism=Schistosoma japonicum"	
ORIGIN	/mol_type="mRNA"	
	/db_xref="taxon:6182"	
	/sex="female"	
	/tissue_type="Whole body"	
	/dev_stage="adult"	
	/lab_host="rabbids"	
	/clone_id="SJF"	
	184 a 112 c 101 g 271 t	
Query Match	23.1%; Score 43.4; DB 13; Length 668;	
Best Local Similarity	53.2%; Pred. No. 14;	
Matches	92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;	
OY	2 TCGACGGATGAGTAAGCTTGATTGCATAATTCGTCCGATTTGCCAGCATTTAAAGC 61	
Dd	667 TCAGCGGTATCGATNACTTGAATTCGAATTCGATTCGGTTGCGACATTTAAGCG 608	
OY	62 TTGACAACCTTTAAAGAAGAAAAGCAAGGTTGAGAAAAGGGTAGTAAAGTATA 121	
Dd	607 GAATTAATCTATTTCCTGAAAGCAAAGCAATACAAATACATCGTTTTATTTAAATCATTTA 548	
OY	122 AGTACAGACC GGAGAGTAGACCGCGGCTCGATTGCTTAAATTTGAAGAAGAA 174	
Dd	547 ACTATTCATCAAAAAACCAACAGTTGATGTAGTTGGTGTGATTAATACGATGAN 495	
RESULT 6		
LOCUS	B5571990	1017 bp DNA linear GSS 17-DEC-2002
DEFINITION	msh2_2193.xl msh Pseudomonas aeruginosa genomic clone msh2_2193,	
ACCESSION	B5571990	genomic survey sequence.
VERSION	B5571990.1	G1:27207051
KEYWORDS	GSS.	
ORGANISM	Pseudomonas aeruginosa	
SOURCE	Pseudomonas aeruginosa	
COMMENT	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.	
REFERENCE	1 (bases 1 to 1017)	
AUTHORS	Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.	
TITLE	Phdome-Genome-Sequencing variation among multiple isolates of Pseudomonas aeruginosa library J Bacteriol., (2002) In press	
JOURNAL COMMENT	Contact: Chris K. Raymond	
	Genome Center	
	University of Washington	
	Box 352145, Seattle, WA 98105-2145, USA	
	Tel.: 2062216954	
	Fax: 2066857244	
	Email: craymond@u.washington.edu	
CLASS	shotgun.	
LOCATION/QUALIFIERS		

```

source
1. .1017
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="M5H"
/db_xref="taxon:287"
/clone="mah2_2193"
/clone_lib="mah"
/notes="Environmental isolate. Whole genomic shotgun
library."
BASE COUNT      203 a      324 c      193 g      294 t      3 others
ORIGIN
Query Match      23.1%; Score 43.4; DB 29; Length 1017;
Best Local Similarity: 69.4%; Pred. No. 13;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 55 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAA 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 GTTGAGAAAGTGGACGGGAGAA 139

RESULT 7
BUT45817      1126 bp      mRNA      linear      EST 10-OCT-2002
LOCUS
DEFINITION
CH2#002_F04T3 Canine heart normalized cDNA Library in pBluescript
Canis familiaris cDNA clone CH2#002_F04 3', mRNA sequence.
BUT45817
VERSION
BUT45817.1 GI:23695391
KEYWORDS
SOURCE
EST.
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Flissipedia; Canidae; Canis.
1 (bases 1 to 1126)
Y.Y., Desai, R., Olathe, M., Henhorn, P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished
Other ESTs: CH2#002_F04T7
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: a1.george@vanderbilt.edu
Insert length: 2104 Std Error: 0.00
Seq primer: T3: ATTACCTCCTCAGTAAGGGA
High quality sequence start: 92
High quality sequence stop: 847.
Location/Qualifiers
1. .1126
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH2#002_F04"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)."
/clone_lib="Canine heart normalized cDNA library in
pBluescript"
/notes="Organ: heart; Vector: pBluescript; Site: 1, 5' of
vector NotI; Site: 2, 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dt primed"
BASE COUNT      279 a      266 c      271 g      310 t
ORIGIN

```

```

Query Match      23.1%; Score 43.4; DB 13; Length 1126;
Best Local Similarity: 66.7%; Pred. No. 13;
Matches 62; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 60.
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 57 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAAAGAGTT 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 GTTGAAACCTTCCACGTTTGATACAAAGAT 149

RESULT 8
CB169458
LOCUS
DEFINITION
RYE602702149.R1 CSEQFLX23 stomach-abomasum Bos taurus cDNA, mRNA
sequence.
CB169458
VERSION
CB169458.1 GI:2815585
KEYWORDS
SOURCE
EST.
ORGANISM
Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 229)
Adelson, D.L. and Gill, C.A.
Bovine ESTs (Adelson and Gill)
Unpublished
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
1. .229
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="stomach-abomasum"
/clone_lib="CSEQFLX23 stomach-abomasum"
/notes="Organ: stomach-abomasum; Vector: pBluescript SK+;
Site: 1: NotI; Site: 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GGAATTGAGCTCCACCGCGGCGGCGCGCGCGAG. sequence 3' of
the inserts (AAGATTCGATTCAGAGCTTATGATACGCTGCGCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
BASE COUNT      61 a      52 c      59 g      57 t
ORIGIN
Query Match      23.0%; Score 43.2; DB 14; Length 229;
Best Local Similarity: 61.6%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 26 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTTAAAGCG 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAAAGAGTTGAAGAGAGGTTAGTAA 112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 AAAGAAAGTGCATTAATTTGTTGAAGCTTTAAAGGAGAGACTTAGAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
BZ561465
LOCUS
DEFINITION
pacs2-164_3275.x4 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_3275, genomic survey sequence.

```

	source	1..269	/organism="Schistosoma japonicum"	
			/mol_type="mRNA"	
			/db_xref="taxon:6182"	
			/sex="female"	
			/tissue_type="whole body"	
			/dev_stage="adult"	
			/lab_host="rabbits"	
			/clone_idb="SJF"	
BASE COUNT	87 a	47 c	42 g	93 t
ORIGIN				
Query Match	Best Local Similarity	22.8%; Score 42.8; DB 13;	Length 269;	
Matches	56; Conservative	0; Mismatches	22; Indels	0; Gaps 0;
OY	1	GTCGACGGTATCGATTACCTTGATATTCGAATTCGTGTCGTTGCAGCATTTAAACGG	60	
Dd	269	GTCGACGGTATCGATTACCTTGATATTCGAATTCGCGCAGACGGGTGATGATGTACGGCT	210	
OY	61	GTTGACAACCTTTAAAGA	78	
Dd	209	ATTCCGAAATTACAAACGA	192	
RESULT 11	BUB02091/c	270 bp	mRNA	linear EST 12-FEB-2003
LOCUS	SJFAD008 SJF Schistosoma japonicum CDNA, mRNA sequence.			
DEFINITION	BUB02091			
ACCESSION	BUB02091			
VERSION	BUB02091.1 GI:28359098			
KEYWORDS	EST.			
SOURCE	Schistosoma japonicum			
ORGANISM	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae; Schistosomatidae; Schistosomatidae; Schistosoma.			
REFERENCE	1 (bases 1 to 270)			
AUTHORS	Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J., Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z., Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han Z.			
TITLE	Expressed sequence tags from female adults of Schistosoma japonicum			
JOURNAL	Unpublished			
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@hgsc.sh.cn.			
FEATURES	Location/Qualifiers			
Source	1..270			
	/organism="Schistosoma japonicum"			
	/mol_type="mRNA"			
	/db_xref="taxon:6182"			
	/sex="female"			
	/tissue_type="whole body"			
	/dev_stage="adult"			
	/lab_host="rabbits"			
	/clone_idb="SJF"			
BASE COUNT	87 a	47 c	42 g	94 t
ORIGIN				
Query Match	22.8%; Score 42.8; DB 13;	Length 270;		
Best Local Similarity	71.8%; Pred. No. 23;			
Matches	56; Conservative	0; Mismatches	22; Indels	0; Gaps 0;
OY	1	GTCGACGGTATCGATTACCTTGATATTCGAATTCGTGTCGTTGCAGCATTTAAACGG	60	
Dd	270	GTCGACGGTATCGATTACCTTGATATTCGAATTCGCGCAGACGGGTGATGATGTACGGCT	211	
OY	61	GTTGACAACCTTTAAAGA	78	

Db 210 ATTCGAATTACAAACGA 193

RESULT 12
LOCUS B2556045 1098 bp DNA linear GSS 17-DEC-2002
DEFINITION pccs1-60_5483.x1 pccs1-60 Pseudomonas aeruginosa genomic clone
ACCESSION B2556045
VERSION B2556045
KEYWORDS B2556045.1 GI:27166248
SOURCE GSS.
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1098)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
Source
Location/Qualifiers
1..1098
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone_lib="pccs1-60_5483"
/clone_1lb="pccs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

BASE COUNT 218 a 325 c 360 g 195 t

ORIGIN

Query Match 22.8%; Score 42.8; DB 29; Length 1098;
Best Local Similarity 68.6%; Pred. No. 17;
Matches 59; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GTTCGACGGTATCGATAGCTGATATCGAATTCGTCGATCGGTGCAGCATTAAAGCG 60
|||||
64 GTTCGACGGTATCGATAGCTGATATCGAATTCGTCGATCGGTGCAGCAGGCGCG 123
|||||

Db 61 GTTGACAACTTTAAAGAGAAAA 86
|||||
124 GGGGACACCATAGACGCAACGAAAG 149
|||||

RESULT 13
LOCUS B2549869 708 bp DNA linear GSS 17-DEC-2002
DEFINITION pccs1-60_2384.x1 pccs1-60 Pseudomonas aeruginosa genomic clone
ACCESSION B2549869
VERSION B2549869
KEYWORDS B2549869.1 GI:27153450
SOURCE GSS.
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 708)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol., (2002) In press

COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
Source
Location/Qualifiers
1..708
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone_lib="pccs1-60_2384"
/clone_1lb="pccs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

BASE COUNT 135 a 194 c 204 g 175 t

ORIGIN

Query Match 22.6%; Score 42.4; DB 29; Length 708;
Best Local Similarity 72.4%; Pred. No. 23;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GTTCGACGGTATCGATAGCTGATATCGAATTCGTCGATCGGTGCAGCATTAAAGCG 60
|||||
52 GTTCGACGGTATCGATAGCTGATATCGAATTCGTCGATCGGTGCAGCAGTCCCGCGCT 111
|||||

Db 61 GTTGACAACTTTAAAG 76
|||||
112 CTTCACCTTCTCAAAA 127
|||||

RESULT 14
LOCUS B0744514 833 bp mRNA linear EST 10-OCT-2002
DEFINITION CH1#002.F10T3 Canine heart non-normalized cDNA library in
pBluescript Canis familiaris cDNA clone CH1#002.F10 3', mRNA
sequence.
ACCESSION B0744514
VERSION B0744514
KEYWORDS B0744514.1 GI:23693350
SOURCE EST.
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 833)
Yi, Y., Desai, R., Olathe, M., Henthorn, P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished
Other ESTs: CH1#002.F10T7
Contact: George A.L.
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1549 Std Error: 0.00
Seq primer: T3: ATTAACCTCCTCAATAAGGA
High quality sequence start: 65
High quality sequence stop: 656.
Location/Qualifiers
1..833
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH1#002.F10"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)."

```

/c1one.lib="Canine heart non-normalized cDNA Library in
pbuescript"
/note="Organ: heart; Vector: pbuescript; Site_1: 5' of
vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dr primed"
BASE COUNT      220 a      175 c      222 g      211 t      5 others
ORIGIN

```

```

Query Match      22.6%; Score 42.4; DB 13; Length 833;
Best Local Similarity 64.0%; Pred. No. 22;
Matches 64; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

```

QY      1  GTGACGGATCGATAGCTTGATATCGAATTCGTCGATTCGTCACGATTAAAGCG 60
          |||||||
Db      30  GTGACGGATCGATAGCTTGATATCGAATTCCTTTTGGTGCAGTCCTGCTCG 89
          |||||||
QY      61  GTTGACAACCTTTAAAGAGAAAGAAAGAGTTGAAGAA 100
          |||||
Db      90  GTTATTATTATAAGCAATTAATTTAGAAAGCAAAATTAA 129
          |||||

```

RESULT 15
BU745422

```

LOCUS      CH1#009_F03T3 Canine heart non-normalized cDNA Library in
DEFINITION pbuescript Canis familiaris cDNA clone CH1#009_F03 3', mRNA
sequence.

```

```

ACCESSION  BU745422
VERSION    BU745422.1 GI:23694771
KEYWORDS   EST
SOURCE     Canis familiaris (dog)

```

```

ORGANISM   Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

```

```

REFERENCE  1 (bases 1 to 958)
AUTHORS   Y.L.Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.
TITLE     Expressed sequence tags from Canine heart
JOURNAL   Unpublished
COMMENT   Other_ESTs: CH1#009_F03T7
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1378 Std Error: 0.00
Seq primer: T3: ATTACCCCTCACTTAAGGA
High quality sequence start: 90
High quality sequence stop: 759.
Location/Qualifiers

```

```

FEATURES
source     1..958
            /organism="Canis familiaris"
            /mol_type="mRNA"
            /db_xref="taxon:9615"
            /clone="CH1#009_F03"
            /tissue_type="heart"
            /cell_type="heart"
            /dev_stage="mixed developmental stages (adult, 30 day - 40
            day fetal)"
            /clone_lib="Canine heart non-normalized cDNA Library in
            pbuescript"

```

```

BASE COUNT      310 a      208 c      166 g      274 t
ORIGIN

```

```

Query Match      22.6%; Score 42.4; DB 13; Length 958;
Best Local Similarity 60.3%; Pred. No. 22;
Matches 70; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```

```

QY      1  GTGACGGATCGATAGCTTGATATCGAATTCGTCGATTCGTCACGATTAAAGCG 60
          |||||||
Db      55  GTGACGGATCGATAGCTTGATATCGAATTCCTTTTGGTGTAAAGAGATTAA 114
          |||||||
QY      61  GTTGACAACCTTTAAAGAGAAAGAAAGAGTTGAAGAAAGGCTAGTAAGTAA 116
          |||||||
Db      115 TTGACAAGTTTCTACTAGCGCAATACCTTAAGAAAGAAATTCGATACAGAA 170
          |||||||

```

```

Search completed: September 26, 2003, 10:15:44
Job time : 2204 secs

```